

FIGURE 1

ACTGCACCTCGGTTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACCGCGTCCGGGCCGGAGCAGCACGGCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCG
CAGCGCTACCCGCCATCGCCTGCCGCCGGCCGCTGGGCTCTGCCGCTTGCTG
CTGCTGCCGCCGCCGGAGGCCAAAGAACGCCACGCCCTGCCACCAGGTGCCGGGGCT
GGTGGACAAGTTAACCAAGGGATGGTGACACCGCAAAGAACAACTTGGCGCGGGAAACA
CGGCTTGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGCGCAGGAGGA
GCACCTGGAGGCCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATCGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCCAGGAACCTACGGTCCCAGTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGAGATGGAGCAGACA
GGCGACGGGTCTGCCGTGCCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTGGGCTGACCAACAGAGACTGCCGGAGTGTGAAGTGGCTGGGTGCT
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCCGCCAGCCGCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCGAGATGTGGACGAGTGTCTCACTAGCAGAAAAACCTGTGTGAGGAAAAACG
AAAACGTACAATACTCCAGGGAGCTACGTCTGTGTGTCCTGACGGCTTCGAAGAAACG
GAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGCGAAGACCTGTAATTGTGCCGACTTACCCCTAAATTATTCAAGAAGGATGTCC
CGTGGAAAATGTGCCCTGAGGATGCCGTCTGCAGTGGACAGCGCGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTCCCTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTGTATATTGATACTGAGTTCTTGTAAATAAAATTGACCATTGTAGGTAAATCAGG
AGGAAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAAC
TTGGCCGCCATGGCCAATTGTTATTGCAGCTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTTCACAAATAAGCATTTCACTGCATTCTAGTTGTGGTTGTCACAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGAATTAAATCGGCCAGCACCATGCCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTAGGTACCTCTGAGGCGAAAGAACCAAGCTGTGGAATG
TGTGTCAGTTAGGGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pi: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPPAPEAAKKPTPCHRGRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNEHTSICTACDESCKTCGTLNRDCGECEVGWVLDE
GACVDVDECAAEPCCSAAQFCKNANGSYTCEEDSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC SLAEKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAAC TG CAC CT CGG TT CT AT CG ATT GA ATT CCC CGGG AT CCT CT AG AG AT CC CT C
GACCTCGACCCACCGTCCGCCAGGCCGGAGGCCACGCCGCCAGCCGTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTCCCGGCAGCGAGGAGGTCTGAGCAGCATGGCCCGGAGGAGGCCCTTC
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGACTGCCGGCGAGGC
CGGCCGCCGCAGGAGGAGGCCTGTACCTATGGATCGATGCTACCAGGAAGAGTACTCA
TAGGATTGAAGAAGATATCCTGATTGTTAGAGGGAAAATGGCACCTTACACATGAT
TTCAGAAAAGCGAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTCTATGAATTCTGTCTTGCGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCTCTGCTGGAACAGTGCCTCACAGGCA
TCAGTTGTTCAAGTTGGTTCCCATGTCCTGGAAAACAGGATGGGTGGCAGCATTGAAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCT
TCTTAAACATGTCAACAAGCTGAGTGCCCAGGCCGGTGCGAAATGGAGGCTTTGTAAT
GAAAGACGCATCTGCAGTGTCCTGATGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCACGATGTATGAATGGTGGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACCTGTGACAAAGCAAACCTGCTCAACCACCTGCTTAATGGAGGAGC
TGTTCTACCTGGAAAATGTATTGCCCTCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACAAACCTGCGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCAGCCTGGCTGGTGACAT
GGAACCTGCCATGAACCCAAACAAATGCCATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGAGC
ACACGCCCTCACTAAAAAGGCCAGGAGCGGCCGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTACAGCCTTGTAACTTCA
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGGCCTGAATTTCATTAGCT
TCATTATAAAATCACTGAGCTGATATTACTCTTCAAGTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTCTTCTGTTCACTGCTTGGACAGATTATATTATGTCATTGA
TCAGGTTAAAATTTCAGTGTGAGTTGGCAGATATTCTAAAATTACAATGCATTATGGT
GTCTGGGGCAGGGAACATCAGAAAGGTAAAATTGGCAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTCAAGATTGTCAGATATTAGAT
GTTGTTACATTAAAATTGCTCTAATTAACTCTCAATACAATATATTGACC
TTACCAATTCCAGAGATTCACTGAGGTTACAGTATTAAAAAAAAAAATTACACTGTGGTAGGGCATT
AAACAATATAATATTCTAAACACAATGAAATAGGAATATAATGTATGAACCTTGCAT
TGGCTGAAAGCAATATAATATTGTAACAAAACACAGCTCTACCTAATAAACATTAT
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTTTGGAAAAA
AAAAAAAAAAAAAAAAAAGGGCGGCCGCACTCTAGAGTCGACCTGCAGAAGCTGGC
CGCCATGGCCCAACTTGTATTGCAGCTATAATG

FIGURE 4

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>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPOLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPHEKALCTPRCMNGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKICPPGLEGEQCEISKCPQPCRNGGKCIKGSKCKCSKGYQGDLCSPKVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACCCGTGGCGTCCGGCGTGGCAGAGCCAGGAGGCCAGGGCGAGGCCAGGGCGGGGCCAGCCTGGG
CCCCAGCCCACACCTCACCAAGGGCCAGGAGCCACC**AT**GTGGCGATGTCCACTGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCACTTGGCTCTGGGTGCCAGCAGGGTCGTGGCGCCGG
GAGCTAGCACCGGGTCTGCACCTGCGGGCATCCGGACGCCGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGCGTGGCAGCAGACTGTGCCCTGCCCTACCTGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGGCGTGCACCCCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGTGCTATCTA
TCCAGTCTGGGAACGTACTGGACAACGTAAACCGTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGGCCCTCTGGGCATGACCTGGAT**TG**AGGGCATTGCTACCGCCTGGCACCA
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATACAGTGTGAACCCAGGGAG
GTGCTTCCCACAGCCTCTGAGGCCCTGTGAGAAGTGGCCAACCTGATTGATGAGCCTTGA
CCAAGGCAACTGTGCAGGCTCCTGGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCCTGTCCTGCGCCCCAGAACCTGCTGTCTTGTGAC
ACCCACCAGCAGCAGGGCTGCCCGGTGGCGTCTCGATGGTGCCTGGTGTCTCGCTCG
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTCGGGCGGTGAACGAGACGGAGGCTGGCC
CTGCGCCCCCTGTATGATGACAGCCAGGCCATGGGTGGGCAAGGCCAGGCCACTGCC
CACTGCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGGAGCTGATGGAGAAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGC
CTTGGGAGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCCGCCACTCCTGGGCC
CAGCCTGGGCCAGAGAGGGCCACTCCGCATCGCGCGCGTCAATGAGTGCACATCGAG
AGCTTCTGCTGGCGTCTGGGCCGCGTGGCATGGAGGACATGGGTATCACTGAGGCTG
CGGGCACCACGCCGGTCCGGCTGGATCCAGGTAAGGGCGGCCAGGAGGCCCAATG
GGCGGTGACCCAGCCTGCCGACAGAGGCCGGCGCAGGCCGGCGCAGGGCGCTAAT
CCCGGCCGGTCCGCTGACGCAGGCCCGCCTGGGAGGCCGCCAGGGCGAGACTGGCG
GAGCCCCCAGACCTCCAGTGGGACGGGCAGGGCTGGCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCTCTGGGCCCTGGACTCAAGACTACCAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATAACCCACCCCAATCCGTATTCTTTTTTTTTAGACAGGGCTTGCTCCG
TTGCCAGGTTGGAGTGCAGTGGCCATAGGGCTCACTGTAACCTCCGACTCCTGGTTCA
AGTGCACCCAGCCCTGTATTCTTCAAGTAGCTGGACTACAGGTGCACCACACCTGGC
TAATTGGTATTTGTAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTCGAACT
CCTGGCTCAAGCGGTCCACCTGCCCTCCCAAAGTGTGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTCAAGATATTATTTCTTCACTGTTAAAAA
AAAAACCAAAAGTATTGATAAAAAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLLCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG
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N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCCTTTCCACAGCAAGCTTNTGCNATCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCGTCTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCTGCCGTGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTGGGCCGTGAACGAGACGAGGCTGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCATGGTCGGGCAAGGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGCCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGCCCTGTCCAAGCCCTATGGAGG
TGCATGAGGACTTCTCCTATAACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTGGG
AGGCCAGAGAGATAACGCCGGCATGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACC CGCGCATCCCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGACCCGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCGAGTGGGAGCCTGTCCTGGTTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCCCTGACCCCTCCCATGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCCTAACCCCTGCTCAGGCACCTCTCCCCCAGGAAGCCTT
CCCTGCCAACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCCGACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCCCTGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTGTTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSDT
DPPADGPSNPLCCCFHGPAGFSTLNPLVRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCACCGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCGCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCCAGATCCGCAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTCAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCAGGAAAGAGCAAAGACTG
CGTGGTCACGGAGATCGTGTGGAGAACAACTATA CGGCCTTCCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCCGCAGGGCGGCCAGGCTTCCGCAGCCGCCAGAAC
CAGCGCAGGCCACTTCATCAAGGCCCTTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAACGAGCAGTCGAGTTGTGGCTCCGCCACCCGCCGACCAAGCGCACAC
GGCGGCCAGCCCTCACGTAGTCTGGGAGGCAGGGCAGCAGCCCTGGCCGCCTCCC
CACCCCTTCCCTTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGAGCCAGATCCCC
GAGGGAGGACCCCTGAGGCCCGAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTCCCCCTCCCGACGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTCAACCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCTGAAGCC
CGCTGAAAGGTCA CGACTGAAGGCCCTGCAGACAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGCCCCAACCTCCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTCA GGAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCACTCCAGCCC
CGGAATAAAACCATTTCTGC

FIGURE 11

MGAARLLPNLTLCQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDGVFTEIVLE
NNYTAFQNARHEGWFMAFRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTCAGTGTGGAAAAATTCTCCCTGTTGAATTTCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTAGCTGGAGTCTGGACTTCAACAGAACCCATCCAGT
CATTTGATTTGCTGTTATTTCCTTTCTTTCCCACCATGTATTAT
TTCCGTACTTCAGAAATGGGCTACAGACCACAAAGTGGCCAGCCATGGGCTTTCC
GAAGTCTTGGCTTATCATTCCCTGGGCCTACTCACAGGTGTCAAACCTCTGGCCTGCC
CTAGTGTGTGCCGCTGCGACAGGAACCTTGCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAAATGC
TGGATTCCTGCAGAACTGCACAAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCAAGAATGTCAGAGTTCTCCATTGCAGGAAAAC
AAATTCAGACCATTTCACGGGCTGCTTGCCTGAAGCTTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCCTCCGGAGGCTATTAGCC
TCAAATTGTTGTTTGCTAAGAATCACCTGAGCAGTGTGCCTGTGGCTCCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATCCGACATGGCCTCCAGAA
TCTCACGAGCTGGAGCGTCTTATTGTGGACGGAACCTCCTGACCAACAAGGGTATCGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTACGTAATTGCTGTCC
CACCCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAGGACAACCAGAT
AAACCACATTCCCTTGACAGCCTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGGGATGCTGACTCAAGGGTTTGATAATCTCTCAAACCTGAAGCAGCTC
ACTGCTCGGAATAACCCCTGGTTTGACTGCAGTATTAAATGGGTACAGAATGGCTCAA
ATATATCCCTTCATCTCTCACGTGCGGGTTCATGTGCCAAGGTCTGAACAAGTCCGGG
GGATGGCCGTCAAGGAATTAAATATGAATCTTTGTCTCTGCCCACGACCCCCGGCTG
CCTCTCTCACCCCAGCCCCAAGTACAGCCTCTCCGACCCTCAGCCTCCACCCCTCTAT
TCCAACCCCTAGCAGAAGCTACACGCCTCCAACCTCTACCACATCGAAACTTCCCACGATT
CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTCTGAACGGATCCAGCTCTATC
CATTTGTGAATGATACTTCAAGTCAGCTGGCTCTCTCTTCAACCGTGATGGCATA
CAAACTCACATGGGTAAAATGGCCACAGTTAGTAGGGGGCATGTTCAAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACCTAGAGCCCCGATCCACCTATCGGATT
TGTTTAGTGCCACTGGATGCTTTAACTACCGCGCGGTAGAAGAGACACCATTTGTTCAAGAGC
CACCAACCATGCCCTCTATCTGAACAAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGATGGGGCGCGGTGATATT
GTGCTGGTGGTCTTGCTCAGCGTCTTGCTGGCATATGCACAAAAGGGCGCTACACCTC
CCAGAAGTGGAAATAACACGGGGCGGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTCAGATCGTCTCCTTAAATAACGAT
CAACTCTTAAAGGAGATTCAGACTGCAGCCATTACACCCAAATGGGGCATTAATTA
CACAGACTGCCATATCCCCAACAAACATGCCGATACTGCAACAGCAGCGTGCAGACCTGGAGC
ACTGCCATACGTGA CAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
CACACTCGTGTGCACATAAAGACACGCAGATTACATTGATAATGTTACACAGATGCAT
TTGTGCATTGAATACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAAGTG
CTATCTTCTATTCAAGTTAAATTACAAACAGTTGTAACTCTTGCTTTAAATCTT

FIGURE 13

MGLQTTKWP SHG AFFL KSWLI ISL GLY SQV SKLL ACPS VCR CDR NFV YCNER SLS TSV PLG IP
EGTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNL PKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLD DNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR
VDENRIAVIS DMAF QNL TS LERL IVD GNLL TNKGIAEGTFSH LT KLEFSI VRNSL SHPPD
LPGTHLIRLYLQDNQINHIPLTA FS NLRKLERLDI SNNQLRMLTQGVFDNLSNLKQLT ARNN
PWFCDCSIK WVT EWLKYIPSSLNVRGFMCQGPEQVRGM AVREL NMNLLSCPTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTSKLPTIPDW DGRERVTPPI SERIQLSIHFVND
TSIQVSWLSLFTVMAYKLTWVKM GHSLVGGIVQERIVS GEKQHLSLVNLEPRSTYRICLVPL
DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFILLAGLIGGA VIFVLVVL
LSVFCWHMHKKGRYTSQWKYNRGRKD DYCEAGTKKD NSILEMTET SFQIVSLNNDQLLKG
DFRLQPIYTPN GGINY TDCHI PNNM RYCNS SVP DLE HCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGAGCAAGGGCGGCGGGAGACAGAGGCAGAGGCAGAAGCTGGGCTCCGTCCCTGCCACGAGCG
ATCCCCGAGGAGGCCGCGCCCTCGCGAGGCCAGAGGCCAGAGGAAGACCGGGTGGCTGCGCCCTGCC
TCGCTCCCAGGCAGGCCCTGCAGCCTGCCCCCTTGCTCGCCTTGAAAATGGAAAGATGCTCGCAGGCT
GCTTTCTGCTGATCCTCGGACAGATCGCCTCCTCCCTGCCAGGGAGGCCAGGGAGCAGTCACTGGGAGG
CTAGGGCAGACAGCTGGACCCACCCGAGACGGCCCTTGAGAGGTTCTGAGAACAAAGCGGGCAGACC
TGGTTTCATCATTGACAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAGGAGGTTCATCGTGGACA
TCTTGCAATTCTTGACATTGGCCTGATGTCAACCGAGTGGCCCTGCTCCAATATGGCAGCACTGTCAAGAATG
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCGTGTCAAGAGGATGCGGCATCTGTCACGG
GCACCATGACTGGCTGGCCATCCAGTATGCCCTGAAACATCGCATTCTCAGAACAGCAGAGGGGGCCGCCCC
GGGAGAATGTGCCACGGGTATAATGATCGTACAGATGGGAGACCTCAGGACTCCGTGGCCAGGTGGCTGCTA
AGGCACGGGACACGGGCATCCTAATCTTGCCATTGGTGTGGCCAGGTAGACTTCAACACCTGAAGTCCATTG
GGAGTGGAGCCCCATGAGGACCATGTCCTGTGGCCAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGCACGGCCACATGTGCAGCACCTGGAGCATAACTGTGCCACTTCTGCACTAACATCCCTG
GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGAGAATCCAGGATCTGT
GTGCCATGGAGGACCAACTGTGAGCAGCTCTGTGTGAATGTGCCGGCTCTCGCTGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGCTGTGACTACTGTGCTCAGAAAACCACGGATGTGAAC
ATGAGTGTGAAATGCTGATGGCTCCTACCTTGCCAGTGCATGAAGGATTGCTCTTAACCCAGATGAAAAAA
CGTGCACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCAGTGCTCAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAAGCCAGTGACCAACTGTGCA
AGCAGGACCATGGCTGTGAGCAGCTGTGTGAACACCGGAGATTCTCGCTGCCAGTGCTCAGAACGGCTTCC
TCATCAACAGGAGGACCTCAAGACCTGCTCCCGGGTGGATTACTGCCCTGCTGAGTGACCATGGTTGTGAATACTCCT
GTGTCAACATGGACAGATCCCTTGCTGCTCAGTGTCTGAGGGACACGTGCTCCGAGCGATGGGAAGACGTGTG
CAAATGGACTCTTGCTCTGGGGACCGGTTGTGAACATTGCTGTAAGCAGTGAAAGATTGCTTGTG
GCCAGTGTGTTGAAGGTTATATACTCCGTAAGATGGAAAACCTGCAAGAGAAAGATGTGCTGCAAGCTATAG
ACCATGGCTGTGAACACATTGTGTGAACAGTGACGACTCATACACGTGAGTGCTGTTGGAGGGATTCCGGCTCG
CTGAGGATGGGAAACGCTGCCAGGAAGGAGATGTCGAAATCAACCCACCATGGCTGCCAACACATTGTTGTTA
ATAATGGAAATTCTTACATCTGCAAATGCTCAGAGGGATTGTTCTAGTGAGGAGCGGAAGACGGTGAAGAAAAT
GCACTGAAGGCCAATTGACCTGGTCTTGATGATGCTGAGGATCTGCAAGAGTCTGGAGAAGAGAATTGAGGTG
TGAAGCAGTTGTCACTGGAATTATAGATTCTGACAATTCCCCAAAGCCGCTGAGTGAGGCTGCTCCAGT
ATTCCACACAGGTCACACAGAGTTCACTCTGAGAAACTTCAACTCAGCAAAGACATGAAAAAGCCGTGGCCC
ACATGAAATACATGGGAAAGGGCTTATGACTGGGCTGGCCCTGAAACACATGTTGAGAGAAGTTTACCAAG
GAGAAGGGCCAGGCCCTTCCACAAGGGTGCCTAGAGCAGGCCATTGTTCTACCGACGGACGGCTCAGGATG
ACGTCCTCGAGTGGCCAGTAAGCCAAGGCCATGGTATCACTATGTATGCTGTTGGGTAGGAAAGCCATTG
AGGAGGAACATACAAGAGATTGCCCTGAGCCCACAAACAAGCATCTTCTATGCCGAAGACTTCAGCACAATGG
ATGAGATAAGTGAAGAAACTCAAGAAAGCATTGTAAGACTCCGATGGAAGACAGGACTCTCAG
CAGGGGAAGTGCACAAACGCCAAGCAAGCAACTCTGAGCCAGTCACCAATAATCCAAGACCTACTTT
CCTGTTCTAATTGTCAGTGCAACACAGATATCTGTTGAAGAAGACAATTTACGGTCTACACAAAGCTT
CCCATTCAACAAACCTTCAGGAAGGCCCTTGGAGAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT
TCCAGAACCTGCAAACGAAGAAGTAAGAAAATTACACAGCGTTAGAAGAAATGACACAGAGAATGGAAGGCC
TGGAAAATGCCCTGAGATACAGATGAAGATTAGAAATCGCAGACACATTGTAGTCATTGATCACGGATTACAAT
GAACGCAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAACAATCAGTACTGA
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTATACTACTAACTTGATAAAATTATCTAGGAAAAAAATCCT
TCAGAAATTCTAAGATGAATTACCAAGGTGAGAATGAATAAGCTATGCAAGGTATTGTAATATACTGTGGACAC
AACTGCTTCTGCCATCTGCCATTGCAATCTCATTGACTATACGATAAAGTTGACAGTCTTACTT
CTGTAGAACACTGCCATAGGAAATGCTGTTTTGACTGGACTTACCTGATATGTATATGGATGTATG
CATAAAATCATAGGACATATGTAACCGTGGATTAAATACAATATTAAATTCAACTTCAG

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPOQTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV
KMRHLSTGTMGLAIQYALNIAFSEAEGARPLRENPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIQVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNPGBFVCQCYSGYA
LAEDGKRCVADYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKPGC
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGEQLCLNTEDSFVCQCSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSRGKTCAKLDSCALGDHGCE
HSCVSSEDSFVCQCFCFGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRRA
EDGKRCRRKDVKSTHGCEHICVNNNGNSYICKCSEGFLAEDGRCKKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIDSILTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFRSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEELQEIASEPTNKHLYAEDFSTMDEISEKLKKGICEALEDSDGRQDS
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEEDNLLRSTQKLSHSTKPGSPL
EEKHDQCKCENLIMFQNLANEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCTCCGGCGTCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCC GGCTGGCGCCCTGACTCCGTCCC GGCCAGGGAGGGC
CATGATTTCCCTCCC GGCCCTGGTGACCAACTTGCTGCGGTTTTGTT CCTGGGCTGA
GTGCCCTCGGCC CCGTGCAGCTGCAACTGCAC TGCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTGCACGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTGATGTGGTTCTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCTCGGGCTGGAGGGTCTCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGCCACAGCATAAAACCT
TAGAACTCAATGTACTGGTCCCTCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCC TGAGCTGCCAGTCTCCAAGGAGTAAGCCC GTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTCCAGACTTCTTGACCAGCATTAGATGT CATCCGTG
GGTCTTTAACGCTCACCAACCTT CGTCTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAGTGAGCACAGGCC TGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGTACCCCTGGTGGACTGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCAACC GCCGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCC TGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGACCC
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCATGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT
GGGGCCCAACCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG
CATGGGTGCTGTCCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTAT**TGATGAC**
CCCACCACTCATGGCTAAAGGATTGGGTCTCCTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTC
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTCCAGTCAGTGAGTCTCCAGGC
CCCCTGATCTGTACCCACCCCTATCTAACACCACCC TTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGGCAGAGGATAGGAAATCTC
TTATTAAGACTAACATGAAATATGTGTTTTCAATTGCAAATTAAATAAGATAACATAA
TGTTGTATGAAAAA

FIGURE 17

MISLGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLP AWYTLHGEVSS
SQPWEVPFVMWFFKQKEKDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEG LQEKGDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKP AVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGT AQC NVTLEVSTGPGAA
VVAGAVVGT LVGLG LLAGLVLLYHRRG KALEEPANDI KEDAIA PRTL PWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPPSLSSQALPS PRLPTTDGAHPQP I SPIPGGVSSSGLSR
MGAVPVMVPAQS QAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCGCTCCTAGTGGTTTTCCACTTG
TTGAATTGTTCTATACTCAAATTGACCCAAGACACCTTGTCTCCAAATGCAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAGGAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGGAAATTAACTCAGTCCTGTGGCAAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGCCATT
TAGATAATGTCGTATAGCTGCAAATATTAATAAAACTTAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAAACA
CTATCTCAGCCAAGGCACCCCTTCTAACTCAACTCTTACTGAATTGTAACCGTGAAT
AATTGTTCAAAGGGATACATTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAATCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTGAT
TCATATAACATGAAACATATTCACTCCTCATATGAATATGGATGGAGACTACATAAATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGAGCTTGCATTGATTTATATT
AGAGTATTGGCTTGTGTTCATCATCTGACAACCTTTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATATGAACATTGAAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGTCATTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATT
TTACAAGGATCACTCAACTAGGAATAATTACTGATTGATTTGCTTGCATATGCA
ACCTTCTGGTCTTCAGTGAATTCAAAGCACCAGGACAACAATTCAAACAAATTCTTGCTG
TAGCCTATTCTTGCTGAACTGTTTTCTTGTGGATCAAATACAAACTAATAAGCTCT
TCTGTTCAATCATTGCCGACTGCTACACTACTTCTTTAGCTGCTTGCATGGATGTGC
ATTGAAGGCATACATCTTCTATTGTTGGGTGTCATCTACAAACAAGGGATTGGCA
CAAGAATTTTATATCTTGGCTATCTAACGCCCAGCCGTGGTAGTTGGATTTCGGCAGCAC
TAGGATACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCAGAAACAACTTATT
TGGAGTTTATAGGACCAGCATGCCTAATCATTCTGTTAATCTCTTGGCTTGGAGTCAT
CATATACAAAGTTTCGTCACACTGCAGGGTGAACCAAGAGTTAGTTGCTTGGAGAACA
TAAGGTCTGTGCAAGAGGGAGCCTCGCTCTGTTCTCTCGGCACCACGGATCTT
GGGTTCTCCATGTTGTGCACGCATCAGGGTTACAGCTTACACTTCAACAGTCAGCAATGC
TTTCCAGGGGATGTTCATTTTTATTCTGTGTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTCAAAATGTCCTGTTGGATGTTAAGGTAAACATAGAGAATG
GTGGATAATTACAACGTGACAAAAAATTTCAAGCTGTGGATGACCAATGTATAAAAAA
TGACTCATCAAATTATCCAATTAACTACTAGACAAAAAGTATTAAATCAGTTTCT
GTTTATGCTATAGGAACGTGAGATAATAAGGTAATTATGTATCATATAGATATACTATGT
TTTCTATGTGAAATAGTTCTGCAAAATAGTATTGAGATATTGAAAGTAATTGGTTT
CTCAGGAGTGTATCACTGCACCAAGGAAGATTCTTCTAACACGAGAAGTATATGAA
TGTCTGAAGGAAACCACTGGCTTGATATTCTGTGACTCGTGTGCCTTGAAACTAGTCC
CCTACCACCTCGGTAAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAACAGAAGGGCAGA
ATATCAAACAGTGAAGGGAAATGATAAGATGTATTGAAATGAACTGTTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAGAACACATTACCACTTGTGAA
TTGTTCTGAACCTAAATGTCCACTAAAACAACCTAGACTTCTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAAAGTTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVVFSTLLNCSYTQNCKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTESYYCMCVPGFRSSSNQDRFITNDGTVCIENVANCHLDNCIAA
NINKTLTKIRSIKEPVALLQEYVYRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL
SNSTLTEREFVKTVNNFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFQKTTEFD
NSTDIALKVFFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSNGNVAVAFLYKSIGPLLS
SSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSRKVTDRYRSLCAF
WNYSPDTMNGWSSEGELTYSNETHTSCRNCNLTHFAILMSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIAGL
LHYFFLAFAFWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVGFSAALGYRYGGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATAATGGATGGAGACTACATAAATATTTCCAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACCTGAAAAATAAACATTTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTCTGGCCTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTTGTCTTGCATATGCATTTACCTTC
TGGTTCTCAGTGAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGTCGGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGCGGGGTACCCCGCTGGGA
CAAGAAGCCGCCGCTGCCCTGCCCGGGGAGGGGGCTGGGCTGGGCCGGAGGCAGG
GGTGTGAGTGGGTGTGCGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGTCTGGGCACCTACCGTGGGGCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG
CCGCCGCGCCGTCAGAGCAGGAGCGCTCGCTCAGGATCTAGGGCACGACCATCCAAACCC
GGCACTCACAGCCCCGAGCGCATCCCGGTGCCGCCAGCCTCCGCACCCCCATGCCGG
AGCTGCCGAGAGCCCCAGGGAGGTGCATGCGAGCGGGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCGGGCGCCCCCTGCCCTCTCGGACGCGGGGCC
CCACGTGCACTACGGCTGGGGGAGCCCATCCGCTGCCGCACCTGTACACCTCCGGGGGG
ACGGGCTCTCCAGCTGCTTCCTGCGCATCCGTGCCGACGGCGTGTGGACTGCCGCCGG
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCTCGGGACCGTGGCCATCAAGGG
CGTGCACAGCGTGCCTGAGCAGTCGCTCTGCCAAACAGCGGCAGCTGTACAAGAA
ACTCGGAGGAAGACTGTGCTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAACGACCGCCTCCGGCTCCCTGAGCAGTCGCTCTGCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTCTCCACTCTCATTTCTGCCATGCTGCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTCTCGCCCTGGAGACCGACAGCATG
GACCCATTGGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCCAGCTTGAGAAGTAA
GAGACCATGCCGGGCTCTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGAGC
TGCTTCTACAAGAACAGTCTGAGTCCACGTTCTGTTAGGAAGAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCCAGTTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGGCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCAGTGTCTAGTTCTGCTGAATACCTCCATCGATGGGAAC
TCACCTCTTGGAAAATTCTTATGTCAAGCTGAAATTCTCTAAATTCTCATCACTTC
CCCAGGAGCAGCCAGAACAGACAGGCAGTAGTTAATTCAAGAACAGGTGATCCACTCTGTA
AAACACGAGGTAATTCACTCAACCCATGTGGAATTGATCTATCTACTTCCAGGG
ACCATTGCCCTCCCAAATCCCTCCAGGCCAGAACAGTGAAGGAGCAGGATGGCCACCG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGGCCCTGGGACAATTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCTCTGAGAATAACTGCTGCCGGTGTACCTGC
TTCCATCTCCAGGCCACCAGCCCTCTGCCACCTCACATGCCCTCCCATGGATTGGGCCT
CCCAGGCCCCCACCTATGTCAACCTGCACCTCTGTTAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTGTCAATAACTGCTGTGGAAGCAGCGGGGAAGACCTAGAAC
CCTTCCCCAGCACTGGTTTCCAACATGATATTATGAGTAATTATTTGATATGTACA
TCTCTTATTCTTACATTATTATGCCCAAAATTATTTATGTATGTAAGTGAGGTTG
TTTGTATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHLRPLVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTGACCTCCTCA
GAGCAGCCGGCTGCCGCCCGGAAGATGGCGAGGAGGAGCCACCGCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGAAAACCCCAA
AGAAGACTGTTCCAGATTAGAGTGBAAGAACTGGTCGGAGTGTCCCTTGCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATAAAAATGTGACAAGAAGTGATGCGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAAATCCAGCTCTGAATACACATGGTTAAGGATGGCATCGTTGCTAGAAA
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAAACTGGAAC
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCCGTGAAGCCCGCAATT
TGTTGGATATCGCAGGTGTCCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGGCCTTAGTGATTCCGTTGTGGCCTGGTATGCTAT
GCTCAGAGGAAAGGCTACTTCAAAAGAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTAAAATGTGCAGTGGCTACGCCTGTAATCCAGCACTTGGAGG
CCGGCGGGCGGATCACGAGGTCAAGACCAGTCTGCCAATATGGTAAACCC
CATCTCTACTAAAATACAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTGAACCCGGAGGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTAAAAAATAAAATAATA
AATAAAACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKT
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD GIRLLENPRLGSQST
NSSYT MNTKTGTIQLQFNTVSKLDTGEYSCEARN SVGYRRCPGKRMQVDDLNISGIIIAVVVVA
LVISVCGLGV CYAQRKG YFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKA AAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTAACATGCTCCACAGCCGGACCCTGGCAT
CATGCTGCTATTCTGAAATACTGAAGAACATGGGATTAAATATTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTACATACTCCACCTTCAAAAAGTACATCAATA
TTATATCATTAAAGGAAATAGTAACCTCTTCTTCCAAATATGCATGACATTGGACAATG
CAATTGTGGCACTGGCACTTATTCTAGTGAAGAAAAACTTGTGGTTCTATGGCATTCA
TTTGACAAATGCAAGCATCTCCTTATCAATCAGCTCCTATTGAACCTACTAGCACTGACTG
TGGAACTCTTAAGGGCCCATTACATTCTGAAGAACAGTAAGATGAAGGACATGCCACT
CCGAATTTCATGTGCTACTTGGCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACTTTCCAGGCCAGATTGCC
AGCTAACACACAGATTCTCTCCTACAGACTAACAAATATTGCAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTACTTGGCTGGATTATCTCAAAACAATTATCTCAGTCACCAAT
ATTAATGTAAGGAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAAACAAACTACTGA
ACTGCCTGAAAAATGTCGTCCAACTGAGCAACTACAAGAACACTATATTAAATCACAACT
TGCTTTCTACAATTCACCTGGAGCCTTATTGGCCTACATAATCTTCTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT
TCTGATGATTGGGAAAATCCAATTATCAGAACATGAACTTTAAGCCTCTTATCA
ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAAGATAACGCCTTGGTT
GGACTGGAAAACCTAGAAAGCATCTCTTACGATAACAGGCTTAAAGTACCCATGT
TGCTCTCAAAGTTGTAATCTCAAATTGGATCTAAATAAAATCCTATTAAATAGAA
TACGAAGGGGTGATTTAGCAATATGCTACACTTAAAGAGTTGGGATAAAATAATGCT
GAGCTGATTTCCATCGATAGTCTGCTGGATAACCTGCCAGATTAAAGAAAATAGAAC
TACTAACAAACCTAGATTGTCTTACATTCCCCAATGCATTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCATGGTCT
CCAAACCTCAAGGAATCAGCATACACAGTAACCCATCAGGTGTGACTGTGTCATCCGTG
GATGAACATGAACAAACCAACATTGATTCATGGAGCCAGATTCACTGTTGCGTGGACC
CACCTGAATTCCAAGGTAGAATGTTGGCAAGTGCATTCAAGGACATGATGGAAATTGT
CTCCCTCTTATAGCTCTGAGAGCTTCTTCTAAATCTAAATGTAAGCTGGAGCTATGT
TTCCTTCACTGTAGAGCTACTGCAGAACACCACAGCCTGAAATCTACTGGATAACACCTCTG
GTCAAAACTCTTGCCTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAAACACTA
GATAAAATGGCGTAACCTCCAAAGAACAGGGGTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG
GCTCTTGAATATTAAGAGATATTCAAGGCCAATTCAAGTTGGTGTCTGGAAAGCA
AGTTCTAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAATTCTCA
TGCTGCCAAAGTGCCTGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTACAGAAAACAGAAAAAAA
TGTGTAAATGTCACCACCAAGGTTGCACCCCTGATCAAAGAGTATGAAAGAATAATAC
CACAAACATTGGCCTGTCTGGAGGCCTCTGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCCAGAAATGAACCTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGATAAAATCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCCT
AAAAACCAAGGAAACCTACTCCAAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVKDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNIAKIEYSTDFFVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELSNLQELYINHNLSTISPGAFIGLHNLLRLHLNSNRQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPPLINLRLSIVAGINLTEIPDNAVLGLENLESISFYDNRL
IKVPHVALQKVNLKFIDLNKNPINRIRRQDFSNMLHLKELGINNMPELISIDSALVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEPDSDLFCVDPPEFQGQNVHQVFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVN VTTKGLHPDQKE
YEKNNTTLMACLGGLGIIGVICLISCLSPEMNCDGGHSYVRNYLQKPTFALGELYPP LIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGGAGTAGATGAGGAATGGGCTCGTATTGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTGTTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTCTCCTCTGGG
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTCAAAGGAGTAGCTGAAACCTTGCAACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAATGCCTCAATAACCTGAAGGCCAGGCCAGAATTGCCAACACCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTGGCTGGTTCACTATGGTGTCTCATATGTGGTATTATGTGAGGCAAATCAGGAG
GATGCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCAATTGAGAAAGAAAGAAA
GTAGTTGCGATTGCACTAGAAATAAGTGGTTACTTCTCCATCCATTGTAAACATTGAA
ACTTTGTATTCAGTTTTTGAAATTATGCCACTGCTGAACTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTTT
AATTAAAAGCAAATAAGCTTAACTTGAACCAGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLCSSSGGLNVTC SANLKEIPRDL
PPETVLLYLDNSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFNKLKARARIANNPWHCDCTLQQVLRSMASNHEAHNVICKTSVLDEHAGR PFL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCAGCAGGGCTGGCAGCCCCATCCTCTGCTGGCT
GGCGTGAGGAGCATGCCAGCCCCCTCTGGCTGCTGGCAGCCCATCCTCTGCTGGCT
GGGCTCAGTGTGTCAGGCTCGGCCACGGGCTGCCGCCCCGCTGCGAGTGCCTCCGCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATAAAAGCTCAACCAGGACGAGTTGCCAG
CTTCCCACCTGGAGGGAGCTGGAGCTCAACGAGAACATCGTAGCGCCGTGGAGGCCGGCG
CCTTCAACAAACCTCTCAACCTCCGGACGCTGGCTCCGCAGCAACCGCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCTCAGCAACCTGACCAAGCAGGACATCGAGAACAAGAT
CGTTATCCTACTGGACTACATGTTAGGACCTGTACAACCTCAAGTCAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCACCGCGCCTCAGCGGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCTGTCCCACCTGCACGGCCT
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCACTTGGACACCATGACACCCAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCGCTTCTCAACCTCTCCTACAACCCCCATCA
GCACCATTGAGGGCTCCATGTTGATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGCG
GGGCAGCTGGCGTGGTGGAGCCCTATGCCCTCCGGCCCTCAACTACCTGCGCGTGTCAA
TGTCTCTGGCAACCAGCTGACCAACTGGAGGAATCAGTCTTCACTCGTGGCAACCTGG
AGACACTCATCTGGACTCCAACCCGCTGGCCTGCGACTGTCGGCTCCTGTGGTGTCCGG
CGCCGCTGGCGCTCAACTCAACCGGCAGCAGCCCACGTGCGCCAGGCCAGTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTTCACCTGCCGCCGCG
CCCGCATCCGGACCGAAGGCCAGCAGGTGTTGTGGACGAGGGCCACACGGTGCAGTT
GTGTGCCGGGCGATGGCAGCCGCCATCCTCTGGCTCTCACCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGGGCAACGCCGGCAACGAC
TCCATGCCCGCCACCTGCATGTGCGCAGCTACTGCCGACTGGCCCCTCAGCCAAACAA
GACCTTCGCTTTCATCTCAACCAGCGGGCGAGGGAGAGGCCAACAGCACCCGCCACTG
TGCCTTCCCCCTCGACATCAAGACCCCTCATCGCCACCACATGGCTTCACTCTTT
CTGGCGTCGCTCTTCTGCCCTGGTGCTGTCTCTGGAGCCGGGCAAGGGCAACAC
AAAGCACAACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG
ACCGCCCGCAAGTTCAACATGAAGATGATA**TGAGGGCGGGCGGGGGCAGGGACCCCCG**
GGCGGGCGGGCAGGGGAAGGGGCTGGCGCCACCTGCTACTCTCAGTCCCTCCACCTC
CTCCCTACCCCTCTACACACGTTCTTCTCCCTCCGCCCTGGCTCCCTGCTGCCCG
CCAGCCCTCACCACCTGCCCTCTTCTACCGACCTCAGAAGCCCAGACCTGGGACCCCCA
CCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACGACACGCCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACCTGGTTCAATAATTATGGATTT
TATGAAAAACTTGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELENENIVSAVEPGAFNNLFNLRTL
GLRSNRLKLIPLGVFTGLSNLTQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVNVSGNQLTLEESVFHSVGNLETLILDSENPLA
CDCRLLWVFRWRNLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPIAILWLSPRKHLVSAKSNGRLTVFDGTLEVRYAQVQDNGTYL
CIAANAGGNDSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCACACGGTCCGCACCTCGGCCCCGGCTCCGAAGCGGCTCGGGGGGCCCTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGCCCCAGCCGCCCGCTCCTGCTCCTGCTCCTGC
TGTTGCCCTGCTGCTGGCGCCCGGCGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGCACCGTGGTGTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTACTTTGGGAGAAGA
GAGCCCTCGAGATAATCGAATTCACTGGTTACCTCTACGCCAACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTT
ATAAAATCTTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTCTGGGAGCAAG
CCTGCAGCCGGCTCACCTGGAGAAAGGGTACCAAGAACCTCACGGAGAACCAACCGCAT
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCAGAACATCTAAAGGGAGCTGAC
AGATCCACCTCTAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAACAGCTGTTGCTACACTGTGAGGGTCGCCGAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCA
CAACATGGGAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTCC
CCTCCTCCAGCACCTACCACGCCATCATCGTGGGATCGTGGCTTCATTGTCTCCTGCTG
CTCATCATGCTCATCTCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCCACAGGGCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGACGACAAGAAGGAATATTCATCTAGAGGCCCTGCCACTCCTGC
GCCCCCGAGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCACCCACCCCGTACAGAACATGTCTGC
TTTGGGTGCGGTTTGACTCGGTTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGTGAGAAAAGCAAAAAACA
AACAAAAACA

FIGURE 32

MGAPAASLLLLLFAACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSIISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDATTNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTCTCCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACTGAATTGTGTCGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAATGGCTGTTGGATTCTGTT
GCTGGAGACGTCTTTGTTGCCGCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCAGTTACCATTATTCATGGCAATT
CCTCACTCGACTTTCCCTAATGAGTCGCTAACCTTATAATGCCGTTAGTTGCACATGG
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTCTGGGCTGCAGCTGGTAAAAGG
CTGCACATCAACAACAAGATCAAGTCTTTGAAAGCAGACTTTCTGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTAAATGACAATCTCATCAGCACCTACCTGCCAAC
GTGTTCCAGTATGTGCCATCACCCACCTCGACCTCCGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCC
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCAGTGGTCTGCAGGCCACAGACTGCAGGGTAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGCTTTGAAAAACCGAGTGGATTCTAGTCTCCGGCGCCCC
CCCAAGAAGAGACCTTGCTCTGGACCCCTGCCAACCTTCAAGACAAATGGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
AAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCAGGAACAAACCTTAGCTAAC
GTTTACCTGCCCTGGGGCTGCAGCTGCACCATCCCAGGGTGGTTAAAGATGAAC
TGCAACAAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCCAAGCTCTAACGTGCAGGA
GCTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTCAAG
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCGGGA
GAAATTCGCGGGCTGAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTAACAAACACCTG
CTGAGGTCCCTGCCTGTGGACGTGTTCTCGCTGGCTCTAACACTCAGCCTGCACAA
CAATTACTCATGTACCTCCGGTGGCAGGGGTGCTGGACCACTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGAGTGCCTGCACAAATGTGCCCTTCAACGAGTGGCA
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTAACCT
TAGAAAGGATTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTACTTCGACAGTAAAACAGCAGCTGGGTTGGCGAGACGGGACGCACTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCGGACTGCTGCTGGT
GTTTGTACCTCCGCCTCACCGTGGTGGCATGCTCGTGTATCCTGAGGAACCGAAAGC
GGTCCAAGAGAGCAGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCCTACAGACAGTCTGT
GAECTCTCCTACTGGCACAATGGCCTTACAACCGAGATGGGCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCAAATAGGGGAGGGCAGAGGGAAGGCG
ATACATCCTTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCGCG
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTCGCACAACCGAAAGGGCCT
GACCCCTTAATTAGCTCCCTCCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTTTGCTGAGAGCCCCTTTGACAGAAAGCCAGCAGCACGCCCTGCTGGAAG
AACTGACAGTGCCTCGCCCTCGGCCCCGGGCCTGTGGGTTGGATGCCGCGGTTCTATAC
ATATATACATATCCACATCTATATAGAGAGATAGATATCTATTCTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAATAAGTAACCTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGVCCKICSCNEIEGDLHVDCCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENGLHEIVPGAFGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLRLDIDPGAFQDLNKLEVLIILNDNLISTLPANVFQYVPITHDLRG
NRLKTLPYEEVLEQIPGIAEILLEDPNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLMETTEQDLCPLKNRVDSSLAPPQEEETFAPGPLPTPKTNGQEDHATPGSAPNGGT
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSDHI PGSGLKMNCCNNRNVSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLLDGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNNAIQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNHYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISV
VPGLLLVFVTSRAFTVVGMLVFLRNRKRSKRRDANSSASEINSLQTVCDSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCCCTGTACCCGGCGCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGACACATTCTGTGCGGGCCTAAGGGAAACTGTTGGC
CGCTGGGCCCGGGGGGATTCTTGGCAGTTGGGGGTCCGTGGGAGCGAGGGCGGAGGGG
AAGGGAGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTCGCTCCTCGAGCGGGACAGATCCAAGTTGGAGCAGCTCTGCGTGCCTGGGCTCAG
AGAATGAGGCCGGCGTTGCCCTGTGCCCTCTGGCAGGCCTCTGGCCGGGCGGCGG
CGGCGAACACCCCCACTGCCGACCGTGCTGGCTGCTCGGCTCGGGGCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGCAGGCGAGGAGGCCTGCATCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGGGGCGAGCTGCGCGCTGTGCTCGCGCTCTGCGGGCAGGCCAGG
GCCCGGAGGGGGCTCAAAGACCTGCTTTCTGGGTGCACTGGAGCGCAGGCCTTCCACT
GCACCCCTGGAGAACGAGCCTTGCAGGGGTTCTCTGGCTGTCCCTCGACCCGGCGGTCTC
GAAAGCGACACGCTGCAGTGGTGGAGGAGCCCCAACGCTCCTGCACCGCGGGAGATGCGC
GGTACTCCAGGCCACGGTGGGTGAGGCCGAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGTACCTGTGCAAGTACCAAGTGGTGGAGGTCTTGTGTCCTCGCCCGCCCCGG
GCCGCCTCTAACTTGAGCTATCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGAATTCA
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTGCA
TCGCAGAACATCGGCCTCGCTGGGACAAACTCTCGGGCGATGTGTTGTGTCCTGCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAAGTGCCTAGACGACTTGGGAGG
CTTGCCCTGCGAATGTGCTACGGGCTTCAGCTGGGAAGGACGGCGCTCTGTTGTGACCA
GTGGGAAGGACAGCCGACCCCTGGGGGACCGGGGTGCCACCAAGCGCCGCCGGCCACT
GCAACCAGCCCCGTGCCGAGAGAACATGCCAATCAGGGTCGACGAGAACGACTGGGAGAGAC
ACCACCTGTCCCTGAACAAGACAATTCAAGTAACATCTATTCTGAGATTCTCGATGGGAT
CACAGAGCACGATGTCTACCCCTCAAATGTCCTCAAGCCGAGTCAGGCACTATCACC
CCATCAGGGAGCGTGAATTCCAAGTTAATTCTACGACTCCCTGCCACTCCTCAGGCTT
CGACTCCTCCTGCCGTGGTCTTCATAATTGTGAGCACAGCAGTAGTAGTGTGTTGGTGT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCAAGAACGCCCCCTTCCAGCCA
AGGAAGGAGTCTATGGGCCGCCGGCCTGGAGAGTGAATCTGAGGCCGCTGCTTGGCTC
CAGTTCTGCACATTGCACAAACAATGGGTGAAAGTCGGGACTGTGATCTGGGACAGAG
CAGAGGGTGCCTTGCTGGCGAGTCCCTCTGGCTCTAGTGATGCAT**AGGGAAACAGGGGA**
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCCTCAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA
TGGTGATACTGGGGACCGGGTAGTGCTGGGAGAGATATTCTTATGTTATTGGAGAA
TTTGGAGAAGTGAATTGAACTTTCAAGACATTGAAACAAATAGAACACAATATAATTAC
TTAAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTCTAGGCTAGGAGTAT
ATTGGTTGAAATCCCAGGGAAAAAAATAAAAATAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPAGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGL
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVIFVSTAVVVLVILTMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDEPAAALGSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGGCTGGGATTCAAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGAAACTAAG
CGTCGAGTCAGACGGCACCATATCGCCTTAAAGTGCCTCCGCCCTGCCGGCCGCGTATC
CCCCGGCTACCTGGGCCGCCCCGGCGCGTGCAGCGCTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCCAGTGTGAGCGCGCGTGTGAGCGCGGGTGGTGCAGGA
GGGGCGTGTGCCGGCGCGCGCGTGGGTGCAAACCCCGAGCGTCTACGCTGCC**ATGA**
GGGGCGCGAACGCCCTGGCGCCACTCTGCCTGCTGGCTGCCACCCAGCTCTCGCG
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTAUTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAATAGCAAATGTAUTGGAAAATCA
CAGTCCCAGAAGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGCCATGCCAATGCCAGCGCATTGGCCG
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC
CCCCAAGTGGCCAGACCGGATTACCTGCAGGAGTCACTTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAAGATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGCCGGGAAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGTAGTCCACCTGCGCAATTGTGTCTGAGAGAAATGAACCTCTTATTCACT
TTTATCAGACTTAAGTTAACGAGTGGGTTATTGGTCACTACATATTGCCAAAAA
AAACTGCCTACAACACTACAGAACAGCCTGTCACCACCATCCCTGTAACCACGGGTTAAA
ACCCACCGTGGCCTGTGTCACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTGTATTAGCCGGCACTGTTACACACCACACTCGCGATGGGAGTTG
CACGCCACAGTCTGATCATCACATCTACAAAGAGGGAAATTGGCGATTCAAGGGCGG
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCTCTCAGAAGAGGTC
TAAATTACATTATTATGCCCAAGTAGGTGAAGATGGCGAGGCAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAACATCAGAACGCTCCTGGATGCCTAAAAAATAAGCAATG
TTAAACAGTGAACGTGTCCTTAAGCTGTATTGCCATTGCTTGAAGATCTATGTC
TCTCAGTAGAAAAAAACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GAAGTGGTGTACTCTCACATGATGGAGGTATGAGGCCCTCCGAGATAGCTGAGGGAAAGTTCTT
TGCCTGCTGTCAAGAGGAGCAGCTATCTGATTGGAAACCTGCCACTTAGTGCAGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGAAGCGTTATTATACATCTGTAAAAGGAT
ATTTAGAATTGAGTTGTGTGAAGATGTAAAAAAAGATTTAGAAGTGCAATATTTATAGT
GTTATTGTTCACCTCAAGCCTTGCCTGAGGTGTTACAATCTGTCTGCCTTCTA
AATCAATGCTTAATAAAATATTTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVLNFRFIDLESNDLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLDRPSGSFKTPNWPD RDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGEVNDARRIGKYCGDSPPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMF KTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCCGGGCTGGGCCTCGCTTCTT
CCTCTCCGTGGCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTACACCTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCGGGACAACCTTGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATAAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTCACAAAGCAGCAGGAGGCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC
CTTCCCTGTCTGGGAAACAGAGAGGCCCTGCGGTGGTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGCACTGTGACTGCCAACGCCGCTACGGGGTGAGGCCTGTGGCC
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTCGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAAGT
GTGGAGCTGACCAATTCTCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGGCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGGAGAGA
ACAAGCAGTGTAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCAGAGATGAC
AGAACAGAGTTGGTGGTGTGCAGCAGATGTTCTTGGCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCAGTTGGTGTACCGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTCAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGA
ATCGCGGCCACCACTGTAGGACCTCCTCCACCCACGCTGCCCGAGAGCTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTGGTTATTTTGAGAGTGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAGAACCC
CCTGAAGGTGGATACCATGAGCTCTCACCTGGGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCTGCCAGTTCTGT
TCTGTGTTCACCACTCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA
AAGGTCTTGGAAAGTTAAAAAAAAAAAAAA

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVC SKSDFECHRLL ESELVESWWFHKQ
QEAPDLFQWLCSDSLKLCGPAGTFGPSCLP CPGGTERPCGGYGC EGE GTRGGSGHCD CQAG
YGGEACGQCGLGYFEAERNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCV DIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACL GCMGAGPGRKKCSPGYQQVGSKCL DVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCAGGGCA
GCACCATGCAGCCCCGTGGCTCTGCTGGCACTCTGGGTGTTGCCCTGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCCAGCTGAGCTCAAAGAGGT
GCCCACCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGCCGCTTCCAGG
AGCCGGTCCCCAAGGCCCGCTGCACAGGCACGGCGCTGTCCCCCGCGAGCGCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCCGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCGAGCCGCTGCTGCTACAGGTGTCGGTGAGAGG
GAGCATCTGGGCCGCTGGCGTCCGGGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC
GCCAGCCGGCTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTGGGGACTATGGAG
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGCCGAGAACTGGGTGCTGGAGCCCCGGGCTT
CCTGGCTTATGAGTGTGGCACCTGCCGGAGCCCCGGAGGCCCTGGCCTCAAGTGGC
CGTTTCTGGGCCTCGACAGTGCATGCCCTCGGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGCAAGGAGGCTCCAGCCATGGCGCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGGTACCGAGAGAGCTG
GCGATGACTGAAGTGCATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTGCTCTCAGGAATGAGAATCTTGCCACTGGA
GAGCCCTTGCTCAGTTCTCTATTCTATTACTGCACTATATTCTAACACTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCATTGTTACTTGTCCGTGAC
TGGATCTGGCTAAAGTCCTCCACCACCACTCTGGACCTAAGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCATCCAGATAATAAGACTTGAAAACATGAATAAAACACATTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGCGGCTTGTCACTGGCCTGATCGCGATGGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTACAGTCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGGAGTGGAAAGTTGACCA
AGGAGACACCACCAGACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG
TGACCTTCTGCCAACCTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCAGCAACAGCTATGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATAACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCAAAAGCACCCGTGCCTCAGCAACTCTCCTATGTCCT
GAATCCCACACAGGAGAGCTGGTCTTGATCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGCATGGAAAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTATTACAGCCAGCCTAGTGCCTGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGTGGCCTGGTCGGCTACCGCCTATCATCTGCATTGCCTTACT
CAGGTGCTACCGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCTTATTGTCCTTC
TACACCCCACAGGGCCCCCTACTTCTCGGATGTGTTTTAATAATGTCAGCTATGTGCC
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACTTGTAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAAATAGGTATCTTGAGCTGGTCTGGCTCTTCTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG
TGATGACACTGGGTCCCTCCATCTCTGGGCCACTCTCTGTCTTCCATGGAAAGTG
CCACTGGATCCCTGCCCTGCCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGGAGCTTGTGGAGAGCAGTAGTAAATTTCAGAGAACTTGAAGCCAAAAG
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAAGACTGGAGGCTGGCGCAGTGGCTACGCC
TAATCCCAGAGGCTGAGGCAGGCAGGATCACCTGAGGTGGAGTCAGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILA ILLCSLALGSVTVHSSEPEVRI PENNPVKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGI VMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGACAGCATGAGCGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG
GCTCGTGCCCACCCACCAAGTTCCAGTGCCGCACCAGTGGCTTATCGTGCCCCTACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCGACTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATTGGGCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC
ACAACCATGGGCCCTGTGACCCCTGGAGAGTGTCCCCTGTGGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCAActGCCTATGGGTTATTGCAGCTGCTGCCGTGC
TCAGTGCAAGCCTGGTACCGCCACCCCTCCTCTTGTCCCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAAC
CTCGCTGCCTGAGGACAAGCACTTGCACCCACCGTCACTCAGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGATCGGATGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAAC
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCDRDLD CSDGSDEEECRIEPCTQKGQC PPPGLPCPCTGVSDCSGGTDKKL
RNCSRLLACLAGELRCTL SDDCIPLTWRCDGHPDCPDSSDELCGTNEILPEGDATTMGPV
LESVTSLRNATTMGPVTL ESVPSVGNATSSAGDQGSPTAYGVIAAAAVLSASLVATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCACCGCGTCGGTCTCGCTCGCGCAGCGGAGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTGTGGATGAAAGATGTTATCATGGAATGAACCCAGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTG
GCCGTGATCCTGTGGTTCAGCTGGCGCTGTGCTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTTCAAGTGTGCTGACCCGGCATTCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTGAAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA
ACAAGACATATAGACATGGAGAGAAGCTAACATCACTTGTATGAAGGATTCAAGATCCGG
TACCCGACCTACACAATATGGTTCATTATGTCGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCGTGAGACCTCTAGCCTCTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT
GATGGGTCTCGGTATCTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGCCACTACCTCCAATGGTGAGTCACGGAGATTCGTCT
GCCACCCGCCCTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTTACTGCGATCCT
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCTCCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGGTGTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCTCCCCGGAG
TTCCAGCAGTGACCCCTGACTTGTGGTAGACGGCGTCCCCGTATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGCTTGAGTGCCTTAGGCCCGGTACATGGCTCTGTGGGCCAG
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTGTGAGCTGCCAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCCCTGCTCGAACCCCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTTGGGAGGTTGATTCCCTTCTTGTGGTTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTTGATCAAGTC
CTGTTCTTCTGACACAGACTGATTAAAAATTAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDFLEQQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSODYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAAEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCACCGCGTCCGCTCCGCCCTCCCCCGCCTCCGTGCGGTCCGTCGGCTAGAGA
TGCTGCTGCCCGGTTGCAGTTGTCGCGCACGCCCTGCCGCCAGCCGCTCCACGCCGT
AGC GCCCGAGTGT CGGGGGCGCACCCGAGTCGGCCATGAGGCCGGAACCCGCTACAGG
CCGTGCTGCTGCCGTGCTGGTGGGCTGCCGCCGACGGGTCGCCTGCTGAGTGCC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTGTTA
TAAAGTCATTTACTTCATGATACTTCTCGAACAGACTGAACTTGAGGAAGCAAAGAACCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTCATTGAAAACCTTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCAGTGA
GGAGAAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT
CACAATTTAGGAACGTGTATGTGGATGAGCCGTCTGCCAGCGAGGTCTGGTGGTCATG
TACCATCAGCCATCGGCACCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACAAATTCAATTGCAAATATTCTGATGAGAAACCAGCAGTTCC
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACAGCTGCCCTGAATCTGGCTACAT
CCTAATCCCCAGCATTCCCCTCTCCTCCTTGTGGTACCAACAGTGTATGTTGGTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAACACACCATC
TGGCCCTCTCCTCACCAGGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCAGACCTGAAGAAATATTCAATTCCGAGTGTGTT
CGGGAGAACCACTCCGATGACATGTCTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAAATGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAACTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC
CTCTTATTTCTATAAGGAAAATACACAGAACGGTCTATGAACAAGCTTAGATCAGGTCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGGACCCCCACGTTGGCTGTATCCTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAACGGTACCTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCACTTGGTTGGTGTATCTAACCTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGGCTGTGGAGCTGGAAAACCACCTCTGTTCTGCTATACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAACATCTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGGAATTCTCATATCTGTTTTCAAAGAAATAAAATCAAATAAAGA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRRGGQPVCRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEADAKKTFKESREAALNLAYILIPSIPLLLLLV
VTTVVVCWWICRKRKREQPDPSKKQHTIWPSPHQGNSPDLEVNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSESGFVTLVSVESGFVTNDIYEFS PDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGTCCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCTACCACCATGATCACTGGTGT
GTTCAAGCATGCGCTTGTGGACCCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTGTTGCTGACACGGGGCTGGAGTCCTCTCAAGCC
GCTCCGCTGGAGGAGCAGGTAGAGTGAAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTGATTACACAGTCACCAATCTAGCTGGTGGCCAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTTGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTC
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTAGAAGTCTTGTATCCAACCTACAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGATAAAAGTGGACTTCTCATCCTCCT
GGACAACGTGGCTGCCAGGCAGCACACAACCTCCAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCTGGGATTTTGACCAAAATGCCACCGTTGCT
GTTGACCTGACCATTGAAACTTACAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACACGGGAAGGAGCAGGTGCCAGAGGGTTGCCCTGATGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSFYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHNLSCPMLKRFARMIEQRAVDTSLYIILPKEDRESLQMAVGPFHLILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTGCAGCTAAACTAAATATTGCTGCTGGGACCTCCTTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTGACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGGCTGGTGGGGCCT
CCACCGCTGTGAAGGGCGGTGGAGGTGGAACAGAAAGGCCAGTGGGACCGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTGCACAGGAACAGAAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTCTTCTCCCCA
GTCCCAGAGGGTGTCAAGGCTGGCTGACGCCCTGGCATTGCAAGGGACCGTGGAAAGTGAA
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGCAAAGGTGG
TGTGCCGGCAGCTGGATGTGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTCA
GGATTGCCCTCTGGCCTTGGGGAAAGAACACCTGCAACCAGATGAAGACACGTGGTCG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG
GAGGTGCTGACAAGGGCTATGGGCTCTGTCTGTGATGACAACCTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGCTGTGGGAAGTCCCTCTCCCTCAGAGACCGGA
AATGCTATGCCCTGGGTTGGCGCATCTGGCTGGATAATGTTCGTTGCTCAGGGAGGAG
CAGTCCCTGGAGCAGTGCACAGATTGGGGTTCACTGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGACTTAACTTGGTGCCTGATTCTCAGGCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAACTACATCA
CCACCTTCCTATGTCTCCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTAT
CAACTACTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCAATTGTCTGTTCTGAAGAACTCTGACAAAATACAGATTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGGTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTATTACAATAATAAGATAGCAC
TATGTGTTCAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCAGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQLMCSGREATLQDCPSGPWGKNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVHKGVWGSVCDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACCGCGTCCCGGGACCGCGTGGGCGGACCGGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCCTGGG
CGTCTTCGGCCTCTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCTACCTGCAGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACACCAGTGGA
TGTGGACAAGAGGGTCACTGGAGACAAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGGAGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCCTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCGGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTCCTGGCTGTTATCTCGAA
CTCTGGCTCCTGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTGAGACTTAATGGAGATTGTCTCACAAGTGGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAGGGCGGCCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCAACTTGTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI
VAAAEEILQCFGYVDIL
VNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKS KNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

FIGURE 58

MKFLLDILLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACCKGLGAKVHTVVDCSNREDIYSSAKVKAEGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCCACGCGTCGGCGACGCGTGGGTGACTAGTTCTAGATCGCGAGCGGCCGCCGC
AGGGAGGAGCACCGACTGCGCCGCACCCCTGAGAGATGGTGGTGCCATGTGGAAAGGTGATTG
TTTCGCTGGTCCTGTTGATGCCTGGCCCTGTGATGGGCTGTTGCTCCCTATA
CAGAAGTGTTCATGCCACCTAACGGGAGACTCAGGACAGCCATTATTCTCACCCCT
TACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTGGTTC
TTCCCAGCTCAGATAACGCCAGAAGATGCCAGTAGTTCTCTGGCTACAGGGTGGCGGG
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGGCTTATGTTGTCACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTACTGATGATAACCCACGGATATGCAGTCATGAGGACGATGT
AGCACGGGATTATACAGTCAGTCAATTCACTAGTTCCAGATATTCTGAATATAAAAATA
ATGACTTTATGTCAGTGGGAGTCTTATGCAGGGAAATATGTCAGCCATTGCACACCTC
ATCCATTCCCTCAACCCCTGTGAGAGAGGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAACAGCAGTGCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAACACTGGATAAAACTACTAGATGGCAGCTAAC
AAGTGATCCTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCGGT
GCACGGAACCTGAGGATCAGCTTACTATGTGAAATTGGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGGAACATAGTTGAAAAGTACTGCGAGA
AGATACAGTACAGTCAGTTAACGCACTGGTTAAGTGAATCATGAATAATTAAAGGTTCTGA
TCTACAATGCCAACGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCTGATGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTACATCCGGCAAGCGGGTGA
CTTCCATCAGGTAAATTATTC
GAGGTGGAGGACATATTTCACCCATGACCAGCCTCTGAGAGCTTGTACATGATTACGA
TTCATTATGGAAAAGGATGGATCCTTATGTTGATAAAACTACCTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATCGAAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTCATCAATAAAAATTATCCTGAAACAAGTGAGC
TTTGTTTTGGGGGAGATGTTACTACAAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
AATTAAAGGTCTTGAATAGGAAGTTTAATTCTCTAAAGAGTAAGTGAAAAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCAAATAAATGGATGAAGCTATAA
TAGTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTGAAATA
AAAATATTATATAAAAGTAAAAAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPKGDSGQPLFLTPYIEAGKIQKGREL
VGPFPGNLMKSYAGFLTVDKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTTSNMTLDRDFPWTTLSMLYIDNPVGTGSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPKREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEKKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGGCTACAAACAT
TTTCCCTTCCTAACAGTTCAACAGCTGTTCAACAGCTAGTGATCAGGGTTCTTCTT
GCTGGAGAAGAAAGGCTGAGGGCAGAGCAGGGACTCTCACTCAGGGTGACCAGCTCCTTG
CCTCTCTGTGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCCTGCCTAACAGCTTCAAAAACAGGAGCGACTTCACTGGCTGGGAT
AAGACGTGCCGGTAGGATAGGAAGACTGGGTTAGTCCTAACATATCAAATTGACTGGCTGGG
TGAACCTAACAGCCTTAACCTCTGGAGATGAAAACGATGGCTAACGGGCCAGAAA
TAGAGATGCTTGTAAAATAAAATTAAAAAGCAAGTATTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGAGGGAGAAAGTATGTTAAAATA
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACCAAGGATGGGACCCCTGGGTC
AGGCCAGCCTTTGCTCCTCCGGAAATTATTTGGTCTGACCACTCTGCCTGTGTTT
GCAGAATCATGTGAGGGCCAACCGGGAAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCTGGAGGTGG
ACAGCCGCTCTGTGGTCCCTGCTCTCAGTGGTCTGGTGCTGGCCCCCAGCAGCCGGC
ATGCCTCAGTTCAGCACCTCCACTCTGAGAATCGTACTGGACCTCAACCAACTTGACCGT
CCACCAAGGGACGGGGCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCTCATCGTGCAGCCCTGCAGCGAAGTGTCAACCAACATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACGCCCTGCTGGCCTGTGGAGCCTCTACCAGGGGTCTGCA
AGCTGCTGCGGCTGGATGACCTCTTACCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCCCTGTCCA
GCCGGAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT
TTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCACTTTGACAT
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGTCTACTTCTACTGTCCAGCCCAGA
CCCTGAGGGTGTGGCATCAACTCCGCTGGAGACCTCTTACACCTCACGCATCGTGG
CTCTGCAAGGATGACCCCAAGTCCACTCATCGTGTCCCTGCCCTGGCTGCACCCGGGC
CGGGGTGGAATACCGCCTCTGCAGGCTGCTTACCTGGCCAAGCCTGGGACTCACTGGCC
AGGCCTCAATATCACCAGCCAGGACGATGTACTCTTGCCATCTTCTCAAAGGGCAGAAG
CACTTACCAACCCGCCGATGACTCTGCCCTGTGTGCCTCCCTACCGGGCATCAACTT
GCAGATCAAGGAGCGCCTGCAGTCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGTCCAGTGCACGAAGGCGCTGTCCCCATCGATGATAACTCTGTGGA
CTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAGGTAAGAGTCTATGAGTTCAAGATGCTCCAATGCC
ATTCACCTCCTCAGCAAAGAGTCCCTTTGGAGGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTTATTTCTGGGAACAAAGGTGAAATGGGGAGGTAAGAAGGGGTTAATTGTTG
ACTTAGCTTCTAGCTACTTCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCTCAAACTTAAGAAAAACTTTAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVVVLLAPPAAGMPQFSTFHSENRDWTFNHLTQHQGTGAVYVGAINRV
YKLIGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTNNVNKLLIIDYSENRLLAGSL
YQGVCKLLRLDDLFLILVEPSHKKEHYLSSVNKTGTMGYVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPKDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHYSVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALECAFPIRAINLQIKERLQSCYQGEQN
LELNWLLGKDQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKGKLVKRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGCGCTGAGTGC GGACTGGAGTGGGAACCGGGTCCCGCGCTTAGAGAACACGCGATGACCA
CGTGGAGCCTCCGGCGGAGGCCGGCCCGCACGCTGGACTCTGCTGCTGGCTTGGGCTTCCTGGCTCC
GCAGGCTGGACTGGAGCACCCCTGGTCCCTCTGCGGCTCGCCATCGACAGCTGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTTCGGGGCTCCATCCACTATTTCCGTGTGCCAGGGAGTACT
GGAGGGACCGCCTGCTGAAGATGAAGGCCTGTTGAACACCCTCACCCACCTATGTTCCGTGGAACCTGCATG
AGCCAGAAAGAGGCAAATTGACTTCTCTGGGAACCTGGACCTGGAGGCCCTCGTCTGATGGCCGAGAGATCG
GGCTGTGGTGAATTCTCGTCCAGGCCCTACATCTGCAGTGAGATGGACCTGGGGCTTGCCAGCTGGCTAC
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTACAAGGGCTTACCGAAGCAGTGGACCTTATTTGACCACC
TGATGTCCAGGGTGGTGCCTCCAGTACAAGCGTGGGGACCTATCATGCCGTGCAAGTGGAGAATGAATATG
GTTCCATAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGGAACCTGC
TCCTGACTTCAGACAACAAGGATGGCTGAGCAAGGGATTGTCCAGGGAGTCTGGCCACCATCAACTTGCAGT
CAACACAGAGCTGCAGCTACTGACCACTTCTCAACGTCCAGGGACTCAGCCAAGATGGTGAATGGAGT
ACTGGACGGGGTGGTTGACTCGTGGGAGGCCCTACAATATCTGGATTCTCTGAGGTTTGAAAACCGTGT
CTGCCATTGAGGCCGGCTCCATCAACCTCTACATGTTCCACGGGACCCAACTTGGCTTCATGAATG
GAGCCATGCACTTCATGACTACAAGTGTCAACAGCAGTCAACTGATGCTGCTGACAGAAGCCGGCG
ATTACACGGCCAAGTACATGAAGCTTGAGACTTCTCGGCTCCATCTCAGGCATCCCTCCCCAACCTG
ACCTTCTTCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTGTACCTGTCTGTGGACGCCCTCAAGTACC
TGGGGAGCCAATCAAGTCTGAAAGGCCATCAACATGGAGAACCTGCAGTCATGGGAAATGGACAGTCCT
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCAATGGGG
TGTTTGTGAACACAGTATCCATAGGATTCTTGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT
ACACCGTGTGAGGATCTGGTGGAGAATCGTGGCGAGTCACATGGGGAGAATATTGATGACCAGCGCAAAG
GCTTAATTGAAATCTCTATCTGAATGATTCAACCCCTGAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCTTCAGAGGTTCGGCTGGACAAATGGNTCCCTCCCAGAAACACCCACATTACCTGCTTCTCTTGG
GTAGCTTGTCCATCAGCTCACGCCCTGTGACACCTTCTGAAGCTGGAGGCTGGAGAACGGGGTTGATTCA
TCAATGGCCAGAACCTGGACGTTACTGGAACATTGGACCCAGAACAGCCTTACCTCCAGGTCCCTGGTTA
GCAGCGGAATCAACCAAGGTACGTTTGAGGAGACATGGCGGCCCTGCATTACAGTCAGGAAACCCCC
ACCTGGCAGGAACCAAGTACATTAAGTGAGCGGTGGCACCCCTCTGCTGGTGCCTGGAGACTGCCCTC
CTCTTGACCTGAAGCTGGCTGCTGCCAACCCCTCACTGCAAAGCATTCTCTTAAGTAGCAACCTCAGGG
ACTGGGGCTACAGTCTGCCCTGTCTCAGCTCAAACCCCTAACGGCTGCAGGGAAAGGTGGATGGCTCTGGCC
TGGCTTGTGATGATGGCTTCTCAAGCCCTGCTCTGTGCGAGGCTGTGCTGGCTGTCTCTAGGGTGGGAGC
AGCTAATCAGATGCCAGCCTTGGCCTCAGAAAAGTGTGAAACCGTGCCTGGAGGACGTACAGCCC
TGCAGCATCTGCTGGACTCAGGCGTGTCTTGCTGGTTCTGGAGGCTTGGCCACATCCCTCATGGCCCC
TTTATCCCCGAAATCCTGGGTGTGTCACCAAGTGTAGAGGGTGGGAAGGGGTGTCTCACCTGAGCTGACTTGT
CTTCCCTCACAAACCTCTGAGCCTTCTTGGGATTCTGGAGGAACCTGGCGTGAAGAACATGTGACTTCC
TCCCTCCACTCGCTGCTCCCACAGGGTACAGGCTGGCTGGAGAACAGAAATCCTCACCTGCGTCTTCC
CAAGTTAGCAGGTGTCTGGTGTGAGTGGAGGACATGTGAGTCTGGCAGAAGCCATGGCCATGTCTGCA
CATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCATGTCTGCA
AGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCATGTCTGCA
GGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCATGTCTGCA
ACAGAACGGCCAGCTCAGTGGCCCCCGCTCCCCACCCCCCAGGCCAGACAGCAGGGCAGAGCAGCCCTCC
GAAGTGTGTCAGTCGCAATTGAGCCTTGTCTGGGCCCCAGCCAAACACCTGGCTTGGCTCACTGTCTG
GTTGCACTAAAGCTATAACCTTGAATCACAA

FIGURE 64

MTTWSLRRR PART LGLLL VV LGFL VL RRL DWST LVPL RL RH QL GL QAK GWN FM LED ST FW
I FGG SI HY FR VP REY WR DR LL KM KAC GL NT LTT YV PW NL HE PERG KF DF SG NLD LEA F VL MA
AE IGL W VIL RP GP YIC SE MDL GG LP SW LL QD PG MRL RT TY KG FTE A VD LY FD HLM SR VV PL Q
Y KR GG PI I AVQ VEN EY GS Y NK DPA Y MP YV KK AL ED RG IVE LLL TSDN KDG LSK GIV QGV LAT
IN LQ S T H E L Q L L T T F L FN VQ GT QP KM VME Y WT GWF D SW GG PH NILD S SE VL KT VSA IVD AGS
S IN LY MF HG GT NF GFM NGAM HF HDY KSD VT SY DY DAVL TEAG DY TA KY MKL RD FF GSIS GIP
L PPP P D L L P KMP YE PL TP VLY LSL WD AL KYL GE PI KSE KPI N M EN L P VNG GNG QSF GY ILY E
TS IT SSG ILS GHV HD RGQ VF VNT VSI GFL DY KTT KIA VPL I QGY TVL RIL VEN RGR VNY GEN
I DD QR KGL I G NLY LND S PLK N FRI Y S LD M KKS FF QRF GLD KWX SL PET PT L PAFF LGS LS IS
S TPC DT FL KLEG W EKG VV FING QNL GRY WNIG P QK TLY LP GP WL SS GIN QV I VFE ET MAG PA
L QFT ET PHL GRN QYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
CTGGTGAGGGTTCTACTTGGCCTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAGG
GGAGCAAAGCCGGCTCGGCCGAGGCCAGGACCTCCATCTCCAATGTGGAGGAATC
CGACACGTGACGGTCTGTCGCCGTCTCAGACTAGAGGAGCGCTGAAACGCCATGGCTCCC
AAGAAGCTGTCTGCCTCGTCCCTGCTGCTGCCGTCAAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTGTTCGTAGTGGATAGGGTCACTGACCGTTCTCCTAGACGGGCC
CGTCCGCTATGTGTCTGGCAGCCTGCACTACTTCGGTACCGCGGGTGCTTGGGCCAC
CGGCTTTGAAGATGCGATGGAGCGGCCCAACGCCATACAGTTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCCTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCATCCTGGTTGCTTCGAAAACCTGAAATTCTAAGAACCTC
AGATCCAGACTCCTTGCGCAGTGGACTCCTGGTCAGAGTCTTGCTGCCAAGATATATC
CATGGCTTATACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTCAGCTACATGAGGCACTTGGCTGGCTCTCGTGCAGTCTAGG
AGAAAAGATCTTGCTCTCACACACAGATGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGG
GAECTCTATACCACGTAGATTTGGCCAGCTGACAACATGACCAAAATCTTACCTGCTT
CGGAAGTATGAACCCATGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
CTGGGGCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTTCCTCCGATTACTACCAAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGACCCACACCTAACGCTTTTGCTCTCGAGATGTACAGCAAGT
TCCAGGAAGTTCTTGGGACCTTACCTCCCCGAGCCCCAAGATGATGCTGGACCTGTG
ACTCTGCACCTGGTTGGCATTACTGGCTTCTAGACTGCTTGCCCCGTGGGCCCAT
TCATTCAATCTTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGACC
GAACCTATATGACCCATACCATTTTGAGCCAACACCATTCTGGGTGCCAATAATGGAGTC
CATGACCGTGCCTATGTGATGGTGGATGGGTGTTCCAGGGTGGAGCGAAATATGAG
AGACAAACTATTTTGACGGGAAACTGGGTCCAAACTGGATATCTTGGTGGAGAACATGG
GGAGGCTCAGCTTGGTCTAACAGCAGTCAAGGGCTGTTGAAGCCACCAATTCTG
GGGCAAACAATCCTAACCAAGTGGATGATGTTCCCTCTGAAAATTGATAACCTGTGAAGTG
GTGGTTCCCTCCAGTTGCCAAATGCCATATCCTCAAGCTCTCTGGCCCCACATTCT
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGTTAACCTGGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCCCTACGTGCCAAGATTCCCTGCTGTTCTAGGGGAGCCCTCAACAAAATTA
CATTGCTGGAACCTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG
TGCCCTGAAACCAATGGAGTTAAGTGGCACTGAAAGTAGGCCGGCATGGCTCATGC
CTGTAATCCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAGGACTTCAAGA
CCAGCCTGGCCAACATGGTAAACCCCGTCCACTAAAATACAAAATTAGCCGGCGTG
ATGGTGGGACCTCTAACCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCAACTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNHYPQPGVNFNGSRLTLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFSYMRHLAGLFRAALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQCNHSTRVSATKGLENMLKLGASVNMYMFHGGSNF
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFALRDVISKFQEVPPLPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFLYRTYMTHTEPTFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLVYPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTGAAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGCTTACATGTTAAAAAGCTTCTCATCAGTTACATATCCATTATTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACCTTGAAGGAATATT
CTTCGAAAAGTCAGAGAAGAGAGCAGTTAGTACATTCCAGATGTCAAAACGATTT
GCGTTCCCTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGAGTTAGTGAAGAAATTAAACTTAGGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTCATG
CTGTCGGGGTGCCCAGTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAATTCTGCTAACGATTCTCAAATGACTAACCTCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGGTGTATTGCTAAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACCTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACATTACAGGAACCTGGAT
TTAAAGTCCAATAACATTGCACAATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTATTACCCATGTCA
AAAACTTGGAGTCACTTATTCTTAACAAACAAGCTCGAACCTTACCAAGTGGCAGTATT
AGTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCATAAAAGTTGAGGACTTGAATCTGGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAAGATCACCTTTGATAACCTGCCACTCGAACGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAAATGGGATTTAAAACTAAGATAATATATGCACAGTGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAAACAGAGAGGATGCATAGAACGGCTGATAGAACACATAACTGAAT
GTTCAATGTTGTTAGGGTTAAGTCATTCAATTCCAAATCATTGTTTTAAATTGTTGTAAC
AAAGGGAAAGGAAAATTATAATCACTAATCTTGGTTCTTTAAATTGTTGTAACGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTTGCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG
VPDAVFDTLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESLSRELRLHILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCELERIPHAIIFSLSNLQELDLKS
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTISSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCLDRPAQLGQCRMLKKSGLVVEDHLFDLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACCGCGTCCGGCCTCTCTGGACTTGCAATTCCATTCCTTCAATTGACAAACTGACTTTTTATTC
TTTTTCCATCTCTGGGCCAGCTGGGATCCTAGGCCGCCCCGGAAAGACATTGTGTTTACACACATAAGGAT
CTGTGTTGGGTTCTTCTTCCCTCCCCTGACATTGGCATTGCTTAGTGGTTGTGCGGGAGGGAGACCACGTGG
GCTCAGTGCCTGCTGCACTTATCTGCCTAGGTACATCGAATCTTGCACCTCCATACAGTGAATTATGCCTGTC
ATCGCTGGTGGTATCTGGGCCCTGCTCCTGCTGATAGTTGTCGTCTGTCTTACTTCAAAATACACAAC
GCGCTAAAGCTGCAAAGAACCTGAAGCTGTGGCTGTAAGGAAACCTACAAACCCAGACAAGGTGTGGTGGCCAAG
AACAGCCAGGCCAAACCAATTGCCACGGAGCTTGTCTGCCCTGCAGTGCTGTGAAGGATATAGAATGTGTGCC
AGTTTGATTCCTGCCACCTGCTGTCGACATAATGAGGGCTCTGAGTTAGGAAAGGCTCCCTCTCAAA
GCAGAGCCCTGAAGACTTCAATGATGCAATGAGGCCACCTGTTGTGATGTGCAGGCCACAGAAGAAAGGCCAG
CTCCCCATCAGTTCATGGAAAATAACTCAGTGCCTGCTGGAAACCAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGCAACCCCTCCAGGAAGGAGTTGGGAGAGAGAACCCACTGTGGGAATGCTGATAAACCAAGTCA
CACAGCTGCTCTATTCTCACACAAATCTACCCCTGCGTGGCTGGAACTGACGTTCCCTGGAGGTGTCAGAAA
GCTGATGTAACACAGAGCCATAAAAGCTGCGTCTTAAGGCTGCCAGGCCCTGCCAAATGGAGCTTGT
AGAAGGCTCATGCCATTGACCCCTTTAATTCTCTCTGTTGGGGAGCTGACAATGGCGGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTGCAATATGGCAGAGACCCACAAAGCCATGATCTGCAACTCAATCCC
AGTGAGAACTGCACTGGACAATAGAAAGACCAGAAAACAAAAGCATCAGAATTATCTTCTATGTCAGCTT
GATCCAGATGGAAGCTGTGAAAGTCAAAGTCTTGACGGAACCTCCAGCAATGGCCTCTGCTAGGG
CAAGTCTGCAGTAAAAGCACTATGTCCTGATTGAAATCATCATCCAGTACATTGACGTTCAAATAGTTACT
GAATCAGCAAGAATTCAAAGAACTGTCCTTGTCTTACTACTTCTCTCCTAACATCTCTATTCCAAACTGT
GGCGTTACCTGGATACCTTGGAGGATCCTTCACCAGCCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT
TGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTCAAAGAGATTTCCTAGAAATAGAC
AAACAGTGCACATTGATTTCCTGCACTCATGATGGCCCTCCACCAACTCTGCCGTGATTGGACAAGTCTGT
GGCGTGTGACTCCCACCTTCAATCTCATCAAACCTCTGACTGCTGTGTTCTACAGATTATGCCAATTCT
TACCGGGATTTCCTGCTTCAACCTCAATTATGCAAGAAAACATCAACACTACATCTTAACCTGCTCTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTAACCTTAATGGAATAACTGCAACTAAA
GACCCAACTGCAGACCAAAATTCAAATGTTGGAATTTCCTGCTCTTAATGGATGTTGACAATCAGA
AAGGTAAGATCAGTCATTACTACACCAATATAATCACCTTCTGATCCTCAACTCTGAAGTGTGATCACC
CGTCAGAAACAACTCCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATAACATAACA
GAAGATGATGTAATACAAGTCAAATGCACTGGCAAAATATAACACCAAGCATGGCTTTGATATCCAATTCA
TTGAAAAGACTATACTGAAATCACCATTATGTTGAAACCAACTCTTTTGTTCAAGTTAGTCTGCAC
ACCTCAGATCCAAATTGGGGTGTCTTGTGATACCTGTAGAGCCTCTCCACCTCTGACTTTGCATCTCAACC
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTTGTAAAGGTGTATCCCTTATTGGACACTATGGGAGA
TTCCAGTTAATGCCTTAAATTCTGAGAAGTATGAGCTCTGTGATCTGAGTGTAAAGTTGATATGTGAT
AGCAGTGACCACCAAGTCTGCTGCAATCAAGGTTGTCTCCAGAAGCAAACGAGACATTCTCATATAATGG
AAAACAGATTCCATCATAGGACCCATTGCTGAAAAGGGATCGAAGTGCAGTGGCAATTCAAGGATTCAGCAT
GAAACACATGCGGAAGAAACTCCAAACCAAGCCTTCAACAGTGTGCACTGTTCTCATGGTCTAGCTCTG
AATGTGGTGACTGTAGCGACAAATCACAGTGAAGGCAATTGTAATCAACGGGAGACTACAAATACAGAAGCTG
CAGAACTATTAACTAACAGGTCCAACCTAAGTGAAGACATGTTCTCCAGGATGCAAAGGAAATGCTACCTCGT
GGCTACACATATTGAATAATGAGGAAGGGCTGAAAGTGAACACACAGGCCCTGCATGTA

FIGURE 70

MELVRRRLMPLTLLILSCLAE LTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ER PENKSIRI IFSYVQLDPDGSCES ENIKVFDGTSSNGPLLQVC SKNDYVPVFESSSSTLT
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMVR II SKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTN II ITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDV IQSQNALGKYNTSMALFESNSFEKTI LESPYVVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFA SPTYDLI KSGCSRDETCKVYPLFGHYGRFQFN AFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVSR SKRDISSYKWKTDSIIGPIRLKRDRSASGN SGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVT VATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCCGGAGCCTGCAGAGAGGACAGCCGGCTGCGCCG
GGAC**ATG**CGGCCCGAGGAGCTCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGC
TGCTGCCGCCGCCGTGCCCTGCCACAGGCCACGCCCTGACCCCCACTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGTGGTTGACCAAGTCGGCATCTTCACTCCACTG
GGGAGTGTTCCTGCCCAGCTCGGTAGCGAGTGGTCTGGTGGTATTGGAAAAGGAAA
AGATAACGAAGTATGTGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT
TTTGGACCACTATTTACAGAAAATTTTAATGCCAACAGTGGCAGATATTTCAAGGC
CTCTGGTGC~~AA~~ATACATTGCTTAACCTCCAACATCATGAAGGCTTACCTGTGGGGGT
CAGAATATTG~~GG~~AACTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGAACAGAACTGACCTGCGTTGGACTGTACTATTCCCTTTGA
ATGGTTTCATCCGCTTCTGAGGATGAATCAGTTCAATTCCATAAGCGGCAATTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACA~~ACT~~TACGCCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGACCCGGATCAAA~~ACT~~TGGAACAGCACAGGCTTCTGGCCTGGTT
ATATAATGAAAGCCCAGTCGGGGCACAGTAGTCACCAATGATCGTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTACCTGCA~~G~~TGATCGTTAAACCCAGGACATCTTGC~~A~~
CATAAA~~TGG~~AAA~~ACT~~GCATGACAATAGACAA~~ACT~~GTCC~~TGGG~~C~~T~~AGGAGGAA~~G~~CTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCA~~ACT~~GTAGAGACAGTTCATGTG
GAGGAA~~AT~~CTTTGATGAATATTGGGCC~~C~~ACACTAGATGGCACCATTCTG~~T~~AGTTTGAG
GAGGCA~~CT~~GAGGCA~~AG~~TGGGCT~~T~~GGCTAAAGTC~~A~~TGGAGAAGCTATT~~T~~TGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCC~~C~~AGATGTGTGGTACACATCCAAGCCTAAAG
AAAATTAGTCTATGCCATT~~T~~TCTAA~~T~~GGCCACATCAGGACAGCTGTC~~C~~TTGGC~~C~~AT
CCCAAAGCTATTCTGGGGCAACAGAGGTGAA~~ACT~~ACTGGGCC~~A~~TGGACAGCCACTTA~~A~~CTG
GATTCTTGAGC~~AA~~ATGGCATT~~T~~GGTAGA~~ACT~~GCCACAGCTAACCA~~T~~CATCAGATGC
CGTGTAA~~AT~~GGGGCT~~T~~GGCT~~T~~AGCC~~T~~AA~~T~~GTGAT**CTAA**AGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGCTAAGGCTAGGA~~ACT~~ATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTA~~AA~~CTGGATAAGAAAATTATTGGCAGTT~~C~~AGCC~~C~~TTCC~~C~~TTTCC~~C~~ACTA
AATT~~TTT~~CTTAA~~TT~~ACCCATGTAACCATT~~TT~~AA~~T~~CTCCAGTGC~~A~~CTT~~G~~CCATTAAAGTC
TCTTCACATTGATTGTTCCATGTGT~~G~~ACTCAGAGGTGAGAATT~~TTT~~CACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGA~~ACT~~GAAAATT~~TT~~TGTTGAAGCC~~A~~TATCCCCATG
ATTATATAGTTATG~~C~~ACTTAATATGGG~~A~~TATT~~TT~~CTGGGA~~A~~ATG~~C~~ATTG~~C~~TAGTCA~~A~~
TTTTTTTG~~G~~CCAACATCATAGAGGTGATT~~TT~~ACAA~~A~~ATCCTAGATGG~~C~~ATAGC~~C~~TACTACA
CACCTAATGTGTATGGTATA~~G~~ACTGTTGCTCTAGGCTACAGACATATA~~C~~AGCATGT~~T~~ACTG
AATACTGTAGGCA~~A~~AGTAACAGTGGTATTGTATATG~~A~~ACATATGGAA~~A~~CATAGAGAGAAG
GTACAGTAAA~~A~~ACTG~~T~~AAA~~A~~ATGGTGCACCTGTATAGGGCA~~T~~ACCACGA~~A~~TGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGA~~A~~GTGAAGGC~~C~~TAGGACATTA
TTGAACACTGCCAGACGTTATAA~~A~~ACTGTATGCTTAGGCTACACTACATTATA~~AAAAAA~~
GTTTTCTTCTTCAATTATAAACATAAGTGTACTGTA~~A~~CTTACAAACGTTAA~~T~~ATT
TTTAAACCTTTGGCTTTGTAATAACACTTAGCTAAAACATAAA~~A~~CTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPCPAHSATRFDPWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSCTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVVRGTVVNTDRWGAGSICKHGGFYTCSDRYNPGLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCATATCACCAAGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGCCAAGGCTCTTGCAGCAGAAGAGCT
TTCCATCCAGGTGTAGCAGAATTATGGGATCACCCCTGTGAGCAAAAGGCGAACCGAGC
AGCTGAATTACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCGGCAAG
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTGAAACTTGCAGCTATGGCTGGGTTGGAGA
TGGATTCGTGGTCATCTAGGATTAGCCAAACCCCAAGTGTGGAAAAATGGGTTGGGTG
TCCTGATTGAAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACACTCATCTGAT
ACTTGGACTAACTCGTCATTCCAGAAATTATCACCACAAAGATCCATATTCAACACTCA
AACTGCAACACAAACACAGAATTATTGTCAAGTACACTACTCCCTGCTCCAGCTTCACTT
ACTCTACAATACTGCCCTACTACTACTCCCTGCTCCAGCTTCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTCAAGAAGTTTATGAAACTAGCACCAGTCTACAGAAC
TGAACCATTGTTGAAAATAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGCAGCTGGTCTGGATTTC
TATGTCAAAGGTATGTGAAGGCTTCCCTTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGA
AAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCCTGGAA
GCTGAAGTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCAGCTGGGAAATCAAAGGGCAAAGAACCAAGAACAGAAAGTCCACCCCTT
GGTCCTAAGTGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAAC
CCTTCTCCTTATTGTAACCCTGCTGGATCCTATCCTCCTACCTCAAAGCTCCCACGGCC
TTCTAGCCTGGCTATGCTTAATAATATCCCCTGAGGAGAAAGGAGTTTGCAAAGTGCAA
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTGAGGCTAGG
TGGGTGAAAGCCAAGGAGTCAGTGGACCAAGGCTTCTACTGATTCCGAGCTCAGAC
CCTTCTCAGCTCTGAAAGAGAAACACGTATCCACCTGACATGTCCTCTGAGCCCGGTA
AGAGCAAAGAACATGGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAAGCTAAAATAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAACACAGACAGGGCAAAGTGTCTCTGAACACATTGAGTTGGA
ATCACTGTTAGAACACACACTTACTTTCTGGTCTCTACCTGCTGATATTCT
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTCTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAATTGACATAGTAGAACGCTATCTGGGAAGCTATTCT
GTTTGATATTCTAGCTTATCTACTTCCAAACTAATTCTATTCTGAGACTAATCTT
ATTCAATTCTCTAATATGGCAACCATTATAACCTTAATTATTAAACATACCTAACAG
TACATTGTTACCTCTATATACCAAAAGCACATTAAAAGTGCCTTAACAAATGTATCACTA
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAAATTAA
AGCATTAGAAAATT

FIGURE 74

MARCFSLVLLTSIWTTRLLVQ GSLRAEELSIQVSCRIMGITLVSKKANQQLNFT EAKEACR
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISP NPKCGKNGVGVLIW KVPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKA AFKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKA PFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGATTGGTGCCCGACTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA
ACTGCCGCCGCTCTGCCACGGTCTGCCAACCCAACGCGAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCCAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAACGGACAAGAGGGTCACTGGATTGTGGAGTTCTTGCAA
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTTGGAAAGGTGGATGTTGGACGCTACTGATGTTAGTACGGGTAC
AAAGTGAGCACATCACCCTCACCAAGCAACTCCCTACCCCTGATCCTGTTCCAAGGGCAA
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTCG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTTCAACCCCCACACAGTGTCA
TGGGAAAACAAGAAGGATAAAAGATCCTCATTGGCAGTGCTCCTCTGTCATT
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTCCCTTGG
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGAAATTGTCAG
GCACCCCTACAGGAAGGCCATGCCATGCTGTGGCCAAGTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGAAATGGTTCCCTCCAAGCTGGTCAGTGTGTTACTGCTTATC
AGCTATTCAAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTTAG
TTGACCTGCACAGCTGGTTAGACCTAGATTAAACCTAAGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCCCCCAAGGACTCTGCTCCTTAAGCCCTTGGCTCGTTATGGTC
TTCATTAAAAGTATAAGCCTAACCTTGTGCTAGCCTAAGGAGAACCTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAAACCCCCCTATTTGTGGGATTGAGAAGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGGTAGGACTTGGAGGAGAAATCCCCTGGACTTCAC
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSPVRLSRWLAQPYYLLSALLSAAFLLVRKLPPCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRTWIVEEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

FIGURE 78

MGLLLLVPLLLLPGSYGLPYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEELDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSDAGPHQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKGHDGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCAGGGGGCGGGGTGCGAGGGATCCCTGACGCCCTGTCCCTGTTCTTGTCGCTCCCAG
CCTGTCGTCGTCGTTGGCGCCCCCGCTCCCCGCGGTGCGGGGTTGCACACCGATCCTG
GGCTCGCTCGATTGCCGCCAGGCGCTCCCAGACCTAGAGGGCGCTGCCCTGGAGCAG
CGGGCGTCTGTCCTCTCCTGCGCCGCCGGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGTGACGCGGGGCCTCCGCACCCCTGGCCTGCCGCATTCTCCCTCTCCAG
GTGTGAGCAGCCTATCAGTCAACCATGTCCGCAGCCTGGATCCCAGCTCTGGCCTCGGTGTG
TGTCTGCTGCTGCTGCCGGGGCCGCGGGCAGCAGGGAGCCGCTCCATTGCTATCACATG
TTTACAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGCTGCC
CTCTGAGGAATTCTCTGTGTATGGAACATAGTATATGTTCTGTATCGAGCATATGTGGG
GCTGCTGTCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCATAGCTACC
TGGTCGAGAAAACATTCTCAGTAGATGCCAATGGCATCCAGTCAAATGCTTCTAGAT
GGTCTGCTCTTCACAGTAACAAAGGAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGTAAACGACTAAAGAAAACACCCGAGAAGAAAACGG
CAATAAAGATTGTAACAGACATTGCATTCTGATTGATGGAAGCTTAATATTGGCAGC
GCCGATTTAATTTACAGAAGAATTGTTGGAAAAGTGGCTCTAATGTTGGAAATTGGAACA
GAAGGACCATGTGGCCTTCAAGCCAGTGAACATCCAAAATAGAATTTCAGGGGTA
AAACTTACATCAGCCAAGATGTTTGTGCAAGGAAAGTAGGTTCAAGGGGTA
ATTCCAATACAGGAAAAGCCTGAAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTATTATTGATGGTGGCCTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGCTGT
CGGAATAATGGCTTCTCTTACACATGCCAAGTGGTTGGCACCACAAAATACGTAAA
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTAACT
CAGTGAACATGCCCTCTAATTGATGGCTCAGCAGTGGAGATAGCAATTGCCCTC
ATGCTGAAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGCAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCAAGTTCACTGACTATAGCACCA
AAGAGAATGTCCCTAGCTGTCACTGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT
GATGCCATTCTTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCTTAGTAATTGTCACAGATGGGAGTCCTATGATGATGTCAAGGCCCTGCAGCTGCTG
CACATGATGCAGGAATCACTATCTCTCTGTTGGTGTGGCCTGGCACCTCTGGATGACCTG
AAAGATATGGCTCTAAACCGAAGGAGTCTCACCGTTCTCACAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGTTAGAGATTCTTAGAATCCCAGCAAT
AATGTAACATTGACAACAGAAAGAAAAGTACAAGGGGATCCAGTGTGAAATTGTATT
CTCATAATACTGAAATGCTTAGCATACTAGAATCAGATAACAAACTATTAAGTATGCAAC
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCCTGTTACAATTACAGTGT
ACTTGTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAA
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCLEEF SVY
GNIVYASVSSICGAAVHRGVI SNSGGPVRYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSDDIEEAGIVAREFGVNFIIVSVAKPIPEELG
MVQDVTFVDKAVCRNNNGFFSYHMPNWF GTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSGDSNFRLMLEFVSNIAKT FEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKD MASKPKESHAFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCCGCGCTCCGCACCGCGGCCGCCCCACCGCGCCGCTCCGCATCTGCACCCGCAGCCC
GGCggcctccggcgggagcgagcagatccagtccggccgcagccaaactcggtccagtcg
GGGCGGCGGCTGCGGGCGCAGAGCGGAGATGCAGCGGCTTGGGCAACCTGCTGTGCCTGC
TGCTGGCGGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGGACCTCGGCTCAGTC
AAGCCGGCCGGCTCTCAGCTACCCGCAGGAGGAGGCCACCCCTCAATGAGATGTTCCGCGA
GGTTGAGGAACTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCAGCTAT
ACAATGAGACCAACACAGACAGAAGGTTGAAATAATACCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGGCCACGAGTGCATCATGCAGCAGGACTGTGGGCCAGC
ATGTAUTGCCAGTTGCCAGCTCCAGTACACCTGCCAGCCATGCCGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA
TGGCCACCAGGGGCAGCAATGGGACCACCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCTTCCAGAGAGGGCTGCTGTTCCCTGTGTGCACACCCCTGCCGTGGAGGGCGA
GCTTGCCATGACCCGCCAGCCGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTTGCCAGTGGCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTCGTGGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC
CAGAGAGTCCCCGATGAGTATGAAGTTGGCAGCTTATGGAGGAGGTGCCAGGAGCTGG
AGGACCTGGAGAGGAGGCTGACTGAAGAGATGGCGCTGGGGAGCCCTGCCGTGCCGGCT
GCACTGCTGGAGGGGAAGAGATTTAGATCTGGACCAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTCCCCAGGTGTGCTTAGGCGTGGCTGACCAGGCTCTTCTACA
TCTTCTCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTGTTCA
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTCTGGAGAGTCAGGCAGGGTTAAAC
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACCAGTTGGCAG
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTCTGATTGGTTGGAAATGTGGAGAAGAGATGCCCTGCTTGCAAAACATCAA
CCTGGCAAAATGCAACAAATGAATTTCACGCAGTTCTTCCATGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACCCCTGCATTACATGTGTTATT
AGCAGTGTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGGAGGGGTATTGTTCTCCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGCCTAACGTACACAGCTAGTGAAGACCAGAGCAGTT
CTGGTTGTGACTCTAACGCTCAGTGCTCTCCACTACCCCCACACCAGCCTGGTGCCACCAA
AAAGTGTCCCCAAAAGGAAGGAGAATGGGATTGGTCTTGAGGCATGCACATGGAATTAAAG
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCGTCTTCTAATGAAGACAATGATATTGACACTGTCCCTTTGGCAGT
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTATAATGAAATTGCAAATCACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTGACAGTTCTTAAAGTTAAAGTTGCACATGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTTGCATTAGAAATCAAGC
ATAAATCACTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLPPSYHNETNTDTKVGNNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG
DQLCVWGHCTKMATRGNSGTICDNQRDCQPGLCQAFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPASCGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAALLGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGGCTGGGAGGAAAGAGGTAAAGAAAGGTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATAATTTCAGCCCATCCACTCTCCTTCCCACACACATGTGCATGTACACACACACATACA
CACACATACACCTCCTCCTTCACTGAAGACTCACAGTCAGTCACTCTGTGAGCAGGTCAAGAAAAGGACAC
TAAAGCCTTAAGGACAGGCCTGGCCATTACCTCTGCAGCTCTTGCTGTGAGTCAGGAAACATGGGAGGGG
CCAGGCACGGTGAACACACTGTAATTCCCAGCATTTGGGAGACCGAGGTGAGCAGATCACCTGAGGTAGGG
TTCGAGACCAGCCTGGCCAACATGGAGAAACCCCCATCTACTAAAAAATACAAAATTAGCCAGGAGTGGTGGC
AGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGATCGCTTGAATCAGGAGGGGAGGATGCAGT
CAGCTGAGTGCACCGCTGCACTCCAGGCTGGGTACAGAATGAGACTCTGCTCAACAAACAAACACGGAGGA
GGGGTAGATACTGCTTCTGCAACCTCCTTAACCTGCATCCTCTTCCAGGCTGCCCTGATGGGGCCTG
GCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGCAGCCCG
GTGTTAGAATGACTGCCCTGGGAGGGTGGTCTTGGGCCCTGGCAGGGTGTGACCCCTACCTGCAAAACACA
AAGAGCAGGACTCCAGACTCCTTGTGAATGGTCCCCTGCCCTGCAAGCTCCACCATGAGGCTTCTCGTGGCCCC
ACTCTGCTAGCTGGTGGCTGGTGCCTGCCACTGCCACTGTGCCGTGGTACCCCTGGCATGTTCCCTGCCCTC
GTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCTGCTCGCCTACCGCGAGGCTACCAACTGTGGACTGCAATGA
CCTATTCCCTGACGGCAGTCCCCCGGACTCCCCCGCAGGACACAGACCCCTGCTCTGCAGAGCAACAGCATTGT
CCGTGTGGACCAGAGTGAAGCTGGCTACCTGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTCGGA
TGCCCGAGACTGTGATTCATGCCCTGCCAGCTGCTGAGCCTGCACCTAGAGGAGAACAGCTGACCCGGCT
GGAGGACCACAGCTTGAGGGCTGGCCAGGCCACAGGAACCTATCTCAACCACAAACCAGCTCTACCGCATCGC
CCCCAGGGCCTTTCTGGCCTCAGCAACTTGCTGCGGCTGCACCTCAACTCCAACCTCTGAGGGCCATTGACAG
CCGCTGGTTGAAATGCTGCCAACTTGAGATACTCATGATTGGCGGAACAAGGTAGATGCCATCTGGACAT
GAACCTCCGGCCCTGGCCAACCTGCGTAGCCTGGTGTAGCAGGCACTGAACCTGCCGGAGATCTCGACTATGC
CCTGGAGGGCTGCAAAGCTGGAGGCTCTCCCTATGACAACCAGCTGGCCGGGTGCCAGGCGGGCACT
GGAACAGGTGCCGGCTCAAGTCTAGACCTCAACAAGAACCGCTCCAGCGGGTAGGGCGGGGACTTGC
CAACATGCTGCACCTTAAGGAGCTGGACTGAACAAACATGGAGGAGCTGGTCTCCATCGACAAGTTGCCCC
GAACCTCCCCGAGCTGACCAAGCTGGACATCACCATAACCCACGGCTGTCCATCCACCCCCCGCCTTCCA
CCACCTGCCCTGAGATGGAGACCCCTATGCTCAACAAACACCGCTCAGTGCCTTGCACAGGAGACGGTGGAGTC
CCTGCCAACCTGCAAGGAGTAGGTCTCCACGGCAACCCATCCGCTGTGACTGTGTATCCGCTGGCCAATGC
CACGGGCACCGTGTCCGCTTCATCGAGCGCAATCCACCCCTGTGTGGAGCCTCCAGCGCCTCCC
GGTCCGTAGGTGCCCTCCGGAGATGACGGACCAACTGTTGCCCTCATCTCCCCACGAAGCTTCCCCCAAG
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCATTGCCGGCACTGGCGAACCCGAACCCGAGATCTACTG
GGTCACTCCAGCTGGCTCGACTGACACCTGCCATGCAGGCAGGAGGTACGGGTGTACCCCGAGGGACCC
GGAGCTGCGGAGGGTGACAGCAGAACAGGGCAGGGCTATACACCTGTGTGGCCAGAACCTGGTGGGGCTGACAC
TAAGACGGTTAGTGTGGTTGTGGCCGTCTCCTCCAGCCAGGGACGAAGGACAGGGGCTGGAGCTCCG
GGTGCAGGAGACCCACCCCTATCACATCTGCTATCTGGGTACCCCAACACAGTGTCCACCAACCTCAC
CTGGTCCAGTGCCTCCTCCCTCCGGGCCAGGGGCCACAGCTCTGGCCCTGCCCTGGGAACCCACAGCTA
CAACATTACCCGCCCTCTCAGGCCACGGAGTACTGGCCTGCCATGCAAGTGGCTTGCTGATGCCACACCCA
GTTGGCTTGTGTATGGGCCAGGACCAAAAGAGGCCACTTCTGCCACAGAGCTTAGGGGATGTCCTGGCTCAT
TGCCATCTGGCTCTCGCTGCCCTCTGCCAGCTGGCTAGCGGCCACCTGGCACAGGCCAACCCAGGAA
GGGTGTGGTGGGAGGGGCCCTCCAGCTGGCTTCTGGGCTGGAGTGCCTGGAGACACTGTGGCC
GTCTGCTCCCTCGTCCTGCCCTGGGAATCCAGGGAGGAGCTGCCAGATCTCAGAAGGGAGACACTGTGGCC
ACCATTGTCTAAATTCTTGAAGCTAGCCTGTCTCAAGTGGAGTACAGTGGACTACTTTTACCAA
AGAGAACAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGGACCCACGTGCTTGAGGCCCTGGCAGCTGGC
CAAGACAGATGGGGCTTGTGGCCCTGGGGGTCTCTGCAGGCCCTTGAAAAAGTTGCCCTTAACCTCTAGGGTCA
CCTCTGCTGCCATTCTGAGGAACATCTCAAGGAACAGGAGGGACTTGGCTAGAGCCTCTGCCCTCCCATCTT
CTCTCTGCCAGAGGCTCCTGGCCTGGCTGTCCCTACCTGTGTCCCCGGCTGCACCCCTTCTCTT
TCTTCTCTGTACAGTCTCAGTTGCTTGTGCTCTGGCAAGGGCTGAAGGAGGCCACTCCATCTCAC
CTCGGGGGCTGCCCTCAATGTGGGAGTGACCCAGCCAGATCTGAAGGACATTTGGAGAGGGATGCCAGGAA
CGCCTCATCTCAGCAGCCTGGCTCGGCATTCCGAAGCTGACTTCTATAGGCAATTGTACCTTGTGGAGAA
ATGTGTACACCTCCCCAACCGATTCACTTTCTCCTGTTGAAAAATAAAATAACAATAAAA
AAAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDNDLFLTA
VPPALPAGTQTLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMMFRPLANRSLVLAGMNLREISDYALEGLQSLSESLSFYDNQ
LARVPRRALEQVPGKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIKFALVNLP
ELTKLDITNNPRLSFIHPRAFHLPQMELMLNNNALSALHQQTVESLPNLQEVLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPMERMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTAGLRLTPAHAGRRYRVYPEGTLELRRTAEEAGLYT
CVAQNLVGADTKTVVVGRALLQPGRDEGQGLELRVQETHPYHILLSWTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWAQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLA AHLGTGQPRKGVGGRPLPPAWAFWGWSAPSRRVV
SAPLVLWPWNPGRKLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGCGCTGTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT
CTACATTGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTACTACGTGCACAA
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCAACCC
CCTGGCCACACTCTCAAGATCCTGGCGTCCTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA
CACACTGTGGTGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTGAGTCGATCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCTCATGCTGCACCTCATGACCAAATACGACCCGCTACTCCAA
GCGCTTCGCGCTTCTGTGGAGGTGAGTGAGAACAGCTGGCGACGTGAACCTCAACAAACGAGTGACGCT
GGACAAGCTCCGGCAGCGGCTACCAAGAACGCCCAGGACAAGCTGGAGCTGCACCTGTCATGCTCAGTGGCAT
CCCTGACACTGTGTTGACCTGGTGGAGGTGAGCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCC
CAGCATTGCCAGCTCACGGCCTCAAGGAGCTGTGGCTCTACACACAGGCCAAGATTGAAGGCCCTGC
GCCCTCCTGCGGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCGCTGTGATCTA
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGCAACCTGAGCGCGGAGAACAAACCGCTACATGTCATCGA
CGGGCTGCGGGAGCTCAAACGCCCAAGGTGCTGCAGCTCAAGAGCAACCTAACGCAAGCTGCACAGGTGGTCAC
AGATGTGGCGTGCACCTGACAGAAGCTGTCCATCAACAATGAGGGACCAAGCTCATCGCCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCACCTGGAGCGCATCCCCACTCCATCTCAGCCT
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGGACATCGAGGAGATCATCAGCTTCCAGCACCT
GCACCGCCTCACCTGCCCTAACGCTGTGGTACAACCACATGCCCTACATCCCCATCCAGATCGCAACCTC
CCTGGAGCGCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTACTGCGCGAAGCTGCG
CTACCTGGACCTCAGCCACAACAACCTGACCTCCCTGCCGACATCGCCTCCTGCAGAACCTCCAGAACCT
AGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTTCCAGTGCAGGAAAGCTGCCGGCTGCACCT
GGGCAACAACGTGCTGCAGTCAGTGCCTCCAGGGTGGCGAGCTGACCAACCTGACGAGATCGAGCTGCCGG
CAACCGGCTGGAGTGCCCTGCCGTGGAGCTGGCGAGTGCCACTGCTCAAGCGCAGCGCTTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCTGAG
GCCGGCCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCCAGGCCGGAGGGCAGGCCAGCTTCTCCAG
AACTCCGGACGCCAGGACAGCCTGCCGGCTGGCAGGAGCCTGGGGCGCTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGGCTGGCCCTTTCTCCCTCTGAGACTCACGCCCCCAGGGCAAGTGCTTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGTCTCTCCCTGGAGGGCCAGCTCTGCCCAAGGGCTGAG
CTGCCACCAGGGCTCTGGGACCCCTACTTTAGTTGGTATTTTTCTCCATCTCCACCTCTTCATCC
AGATAACTTATACATTCCAAGAAAGTTAGCCAGATGGAAGGTGTTAGGGAAAGGTGGCTGCCTTTCCCC
TTGTCTTATTAGCGATGCCGCCGGCATTTAACACCCACTGGACTTCAGCAGAGTGCTGGGGCGAACCA
CCATGGGACGGTCACCCAGCAGTGCCGGCTGGCTCTGCCGTGCCACTGGAGAGCAGGCCCTCAGCTGGA
AAGGCCAGGCCGGCTGGAGCTGCCTCTCAGTTTGCGAGTTTTAGTTTTGTTTTTTTAATCAAA
AAACAATTTTTAAAAAAAAGCTTGAAATGGATGGTTGGGTATTAAAAAGAAAAAAACTTAAAAAAA
AAAAGACACTAACGGCCAGTGAGTTGAGTCTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAAGCAGGCCAGACGT
TGAACGTGTTCCCTTCCCTGGCGCAGGGTGCAGGGTCTTCCGGATCTGGTGTGACCTTGGTCCAGGAGTT
CTATTGTTCTGGGAGGGAGGTTTTTGTTGTTGGTTTTGGTTTTGGTGTCTTGTGTTCTTCTCC
ATGTGTCTTGGCAGGCACTATTCTGTGGCTGCGCCAGAGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTGGCTAATCCCCGATGAACGGTGCTCCATTGCCACCTCCCTCCTGCCCTGCCCTC
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTTCGCCAGACTTGTGTTCCCCACCTCCTGCCATGGGTGT
CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTCGCCACCTGGCTCTCATGAAGAGCAGACACTTA
GAGGCTGGTGGGAATGGGAGGTGCGCCCTGGGAGGGCAGGCAGGGTGGTCCAGGCCGGTCCCGTCCCTGGCGC
CTGGAGTGACACAGCCAGTCGGCACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTT
AGAAGGGTCCCCGCCCTAGATCAATCAGTGGACACTAAGGCACGTTTAGAGTCCTTGCTTAATGATTATGT
CCATCCGTCTGTCGTCCATTGTGTTCTGCGTGTGTCATTGGATATAATCCTCAGAAATAATGCAACTAG
CCTCTGACAACCATGAAGAAAAATCGTTACATGTGGGTCTGAACITGTAGACTCGGTACAGTATCAAATAA
ATCTATAACAGAAAAAAA

FIGURE 88

MRQTIIVIKFILIIICYTVYYVHNIKFVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNNEWTLDKLQRQLTKNAQDKLELHLFMLSGIPDTVFVFLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENRLRALHIKFTDIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPPELFQCRKLRALHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCCGCTGCTGGCCTGAACGCAGGAGCTGTCAATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGGCGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGGCACTGGTTCAAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTCTCCTGAAGACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCACCTTGCGGGGT
TGCCTTGGGTGATTCTGGATCTCCCTGTTGATTGGTCTCTCCTGGGACCTTACCTGT
ACAGCATGTCTCTCTCGAACGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTGTCTTGTAGCGC
CACGTGAGACACCTACAAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAATTATTCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTAGGAGGCCTG
GGTGGGAAACTGAAGTGGCAGAACTGCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCCCTGT
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTATATGGTTCTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTACTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGGCTGTGATCAAGAACGGTCTGACCAAGCTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTCCTGCTTCTAAAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELGKAEMIIEQNTDGVNFYNLTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQOE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGC~~GGGAGAGGAGGCC~~**ATGGCGCGCGCGCTGCTGGCGCTGCTGGCTC**
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGC~~GGCCGA~~
CGGGTCATCACGT~~CGGCATCGTGGTGAGAGGACGCCA~~CTCGGGCTGGCGTGGCA
GGGGAGCCT~~GCCTGTGGGATTCCCACGTATGCGGAGT~~GAGCCTGCTCAGCCACC~~GCTGGG~~
CACTCACGGCGCGCACTGCTTGAAACCTATAGTGACCTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGCCAGCTGACTTCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCACCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGT~~CACCTACACTAAACACATCCAGCCC~~ATCTGTCTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTT~~CAGGTGCCATCATAAACAA~~
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG
GTTTGTGCTGCCAACGCCAAGGCGGGAGGATGCCTGCTCGGTGACTCAGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGCCCAATCGGCCGGTGT~~ACACCAATATCAGCCACC~~ACTTTGAGTGGATCCAGAAG
CTGATGGCC~~CAGAGTGGCATGTCCCAGCCAGACCCCTC~~TGGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCCTGGGCCGGT**CTGAGCCTACCTGAGCCC**ATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTCTCTGTCTTGGTAATAAACACATTCCAGTTGA
TGCCTTG~~CAGGGCATTCTCA~~AAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCGVSLLSHRWALTAACFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACACGGTCCGGACCGTGGGAAGGGCAGAATGGACTCCAAGCCTGCCCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCGGAGCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGTCCCTGGGCCGTGCGGACCCGTGAGGAAGAGCTGAGTCTCACCTT
GCCCTGAGACAGCAGAAATGTGAAAAGACTCTCGGAGCTGGTCAGGCTGTGTCGGATCCCAG
CTCTCCTCAATAACGGAAAATACCTGACCTAGAGAAATGTGGCTGATCTGGTAGGCCATTCC
CACTGACCCCTCACACGGTGCAAAATGGCTCTTGGCAGCCGGAGGCCAGAAGTGCCATTCT
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGCTGAGTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCTGGCCCCCATGTGGACTTTGTGGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCCCTGTGATCCGTAAAGCGATAACAACCTGACCTACAAGACGTGG
GCTCTGGCACAGCAATAACAGCCAAGCCTGTGCCAGTTCCCTGGAGCAGTATTCATGAC
TCAGACCTGGCTCAGTCATGCCCTTCGGTGGCAACTTGCACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGATTGAGGCCAGTCTAGATGTGCACT
ACCTGATGAGTGCTGGTGCACATCTCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTTCCTGCAGTGGCTCATGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCTACATCCAGCGGTCA
ACACTGAGCTCATGAAGGCTGCCCTGGGTCTCACCTGCTCTCGCCTCAGGTGACAGT
GGGGCGGGTGTGGCTGTCTGGAAAGACACCAGTTCCGCCCTACCTCCCTGCCTCCAG
CCCCTATGTCACCACAGTGGGAGGCACATCCTCAGGAACCTTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCCACGGCCTCATACCAGGAG
GAAGCTGTAACGAAGTCCCTGAGCTCTAGCCCCCACCTGCCACCATCCAGTTACTCAATGC
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCCATCCATGGGTGTCCGGAACCTCGGCCTCTACTCCAGTGTGTTGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTAGTGGCCCCCCCTTTGGCTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGCAGGTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGATCCTGTAACAGGC
TGGGAACACCAACTCCAGTTGCTGAAGACTCTACTCAACCCCTGACCCCTTCTATC
AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTCACTTCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
TGCTGTGAGCTTGACTTCACTCCAAACCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCTTAGATTCTCAATAAGATGCTGTAACTAGCATTGGATGCTCTCCCTCCGC
ATCTCATCTTCTCTTCAATCAGGCTTCCAAAGGGTTGTATACAGACTCTGTGCACTA
TTCACTTGATATTCAATTCCCCAATTCACTGCAAGGAGACCTCTACTGTCACTGTTACTCT
TTCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTCTCAATCTTGTGTTATG
GCCTTCCATCATAGTTGCCACTCCCTCTCCTACTTAGCTCCAGGTCTTAACCTCTG
ACTACTCTTGCTTCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTGC
TCCATTGTAGATTTGCTCTCAGTTACTCATTGCTCCCTGGAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAAGACTTCTATCCAATAATGATTGATACTCAAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRTLPPGVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSCTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEPFLQWMLM
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAARGLTLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GCCGCGCGCTCTCTCCGGGCCACACCTGTCTGAGCGGCAGCGAGCCGGCCGGC
GGGCTGCTCGCGCGAACAGTGTCTGGCATGGCAGGGATTCCAGGGCTCCTCTC
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTACAGTGCCCCCTGAAACCCACTG
GCCTGCATACCGCCTCCCTGCGTCTGCCCAAGTCTACCCCTCAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCAGTGTATAAGGAAACT
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAAAGGACTTCCTGCTCAACTACCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCCCTGGTGGCAGAGAACGATGTCCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAACGCTTCAGCCATGCCAGCAGATGAA
AAGTTAAAGATGGTGGTCGAGGGCCAACGACTCCACTTCAGCCATGCCAGCAGATGAA
ATTCAGTGGATCCGGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACTCAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGTGAGCCCTCTGCTAAGCAGCTGCCAGGGGCCAGGGTCTGGGTCTAT
TGGTTATGACAATGACCGACCAGGAATTGGTGTATGCTCTGTGACGTCAAAGACGAGA
CCTATGACTGCTCTACCAGCAATGCGATGCCAGCCAGGGCCAGGGTCTGGGTCTAT
GTGAGGATGTGAAGAGACAGCAGCAGAAGTGGAGCGAAAAATTATTGGCATTTCAGG
GCACCAGTGGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAGAATCACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG
TGACACAGTGTCCCTCTGGCAGCAATTAGGGTCTCATGTTCTATTAGGAGAGGCC
AAATTGTTTTGTCAATTGGCGTGCACACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
CTTATAATCTTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAAATG
GTTTGTGTATCATATCATATCATTTAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTGGGCAATGAGGAATATTGACAATTAGTTAATCTTCACGTTTG
CAAACTTGATTTCATCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRD
SGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTIVAEKHVLTA
AHCIDHGKTYVK
TQKLRVGFLKPDKFDGGRGANDSTSAMPEQMFKFQWIRVKRTHVPKG
WIKGNA
NDIGMDYDYA
LLELKPKH
RKFMKIGVSPPAKQLPGGR
IHFS
GYDNDRPGNLVYRFCDVKDETYDLLYQQCD
AQPGASGSGVYVRM
WKRQQQKWERKIIGIFSGHQ
WVDMNGSPQDFNVAVRITPLKYA
QICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCACCAGCCATGGTGGTT
CTGGAGCGCCCCAGCCCTGGGTGGGGCTGTCTCGGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGGCGGCAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCCTGGCTCTCGTCCCAGAAGGTGGGTGTTGCCCTGGTGGAGC
CCCACCCCTGTATTCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCCTCAGACCCTGCAGAACGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCCCTATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGCGAGGGCTGTGCCGAGCGAACAGGCC
GGGGTCTACATCAGCCTCTCGCGACCGCTCCTGGGTGGAGAACGATCGTCAAGGGGTGCA
GCTCCCGGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCCG
CCGCGCCTTAGGGCGCAGCGGACGCGGGCTCGGATCTGAAAGGCGCCAGATCCACA
TCTGGATCTGGATCTGGCGGGCTCGGGCGTTCCCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTCGGAAAGGAAACCCCTCCCCGACCGCCCGAC
GGCCTCAGGCCCTCCAAGGCATCAGGCCGCCAACGGCTCATGTCCCCGCCAAC
GACTTCCGGCCCCGCCCCGGGCCAGCGCTTTGTGTATATAATGTTAATGATTATTAT
AGGTATTTGTAACCCTGCCACATATCTTATTATTCTCCAATTCAATAATTATTATT
CTCCAAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQQLNRRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGII SWGEGCAERNRPGVYISLSAHRSWEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCTGCAGTTCTGATGCTTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGCCAC
AACAAAGGAGCGCGGGCGCCGCGAGAATCTTCGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGACCT
GCAGCCCAGGCCAGATGTGCCGCACACTACGCAGGTGGTATGGCCAAGACAGAGAGGATC
GGCTGTGGTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGGCCCTACCAGGAGGGACTC
CGTGCCTCCAAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTGCCCTACCTGGTAACGTGAGGCCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTCCCTAGCAACGGGGATTCCGGCTTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCCTGTGGAAACCCAGGCC
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTGCGTAAC
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTGGATGAGGAGGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGGCCAGAGAACTCTGGACCCCCAAGATGTCCCTGACAGGGCAAG
GGAACCTCCTACCCATGCCAGGGAGGCTGAGGCTGAGTGCCTCCCTCAGTG
AGGTCTTGGCCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCCTGCCAGGTGCAGAGGGCCCTGACA
AGCCTAGCGTTGTGTAGGGCTGAACCTGGGCCCTGGTCATGTGTGGGCCCTCTGGGA
CTACTGCTCCTGCCCTCTGGTGTGGCTGGAATCTTCTTGAATGGATACCAACTCAAAGGG
TGAAGAGGTCACTGTCCTCTGTGATCTTCCCCACCCCTGTCCCCAGCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCGGAAGGGAAAGGCTACGGGCATGTGCCTCATCACACCCTCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCTCCCTGCCCTCCCTCCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT
CACTGCCTACCTGGCCTGGGCTGTCTGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTTC
TTTGAGTGGGGAGGCAGGGACGGAGGAAAGTAACCTCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLPLLLLATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVGHNKERRRGENLFAITDEGMVDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPyQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPYLVTTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAHSLPSLDEEPVTFPKS
THVPIPDKSADKVTDKTKVPSRSPENSMDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVWGPLLGLLLLPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACGTGAAAGTCAGGCTTTCATTTGGGAAGCCCCCTAACAGAATTGGTCACTTCTCCAAGTTATGGTGGACGT
ACTTCTGTTGTTCTCCCTCGCTTGCACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTTCAT
CAAGGCAGTTCCATGAGCACCTTCAAAGCCTCGAGAAGTGAACAAACAAATGAATTGGAGACCATTCC
AAATCTGGGACCAGTCTGCCAAATATTACACTTCTCCTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
ACATCTGAAAGAGTTCACTGCCCCGAAACTTGGACCTTAGCAGCAACAATATTCAAGAGCTCCAAACTGCATT
TCCAGCCCACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTGACAA
TTTGGCCAACACACACTCCTTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAAGATGTTAAACT
GCCCAACTGCAACATCTCGAATTGAAACGAAACAAGATTAATAATGAGATGGACTGACATTCAAGGCCCTGG
TGCTCTGAAAGTCTGAAAATGCAAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAA
CATGGAAATTTTGAGCTGACCATAACAAACCTAACAGAGATTACCAAAGGCTGCTTACGGCTTGCTGATGCT
GCAGGAACCTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGCTCTGCCAGAACGCTCAG
TGAGCTGGACCTAACATTCAACTTCAAGGTTAGATGATTCAAGCTTCTGGCTAAAGCTTACTAAATAC
ACTGCACATTGGAAACAACAGAGTCAGCTACATTGCTGATTGCTGCTTCCGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAAGAACAAATGAAATTTCCTGGACTATTGAGACATGAATGGTCTTCTCTGGGCTTGACAAACACTGAG
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCATTGGAGCA
TCTAGACCTGAGTGACAACGCAATCATGTTACAAGGCAATGCATTTCACAATGAAGAAAATGCAACAAATT
GCATTAAATAACATCAAGCCTTGTGCGATTGCCAGCTAAATGGCTCCCACAGTGGTGGCGAAAACAACTT
TCAGAGCTTGTAATGCCAGTTGTGCCATCCTCAGCTGCTAAAGGAAGAAGCATTGGCTGTTAGCCAGA
TGGCTTGCTGTTGATGATTTCACAGGAAACCCAGATCACGGTTCAAGCCAGAAACACAGTCGGCAATAAAAGGTT
CAATTGAGTTCATCTGCTCAGCTGCCAGCAGCAGTGCATTCCCAATGACTTTGCTTGGAAAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCAAGGTGGCAGGGTATGGAGTATACCAC
CATCCTCGGCTGCGCAGGGTGAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCCAATCATTGGTTC
ATCCTACTCTGTCAAAGCAAGCTTACAGTAAATATGCTTCCCTATTCAACAGACCCCCATGGATCTCACCCT
CCGAGCTGGGCCATGGCACGCTGGAGTGTGCTGCTGCTGGGACCCAGCCCCCAGATAGCCTGGCAGAACGGA
TGGGGCACAGACTTCCAGCTGCACGGGAGAGACGCATGATGATGCCGAGGATGACGTGTTCTTATCGT
GGATGTGAAGATAGAGGACATTGGGTATACAGCTGCACAGTCAGAACAGTGCAGGAAGTATTCAGCAAATGC
AACTCTGACTGTCCTAGAAACACCATCATTGGCCACTGTTGGACCGAAGTGAACCAAGGGAGAAACAGC
CGCCTACAGTGCTGTTGGGACGGAAAGCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGT
AACCGAGAGGACTTTTGAGCAGCAGGAATCAGCTCTGATTATTGTTGACTCAGATGTCAGTGATGCTGGAA
ATACACATGTGAGATGCTAACACCCCTGGCAGAGAGGAAACGTCAGGCTCAGTGATCCCCACTCCAAC
CTGCACTCCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCACTGTTGGGTGCTGATCATAGC
CGTGGTTGCTGTTGGGACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGA
TTGCAGCATTACCAACACAGATGAGACCAACTGCCAGCAGATATTCTAGTTATTGTCATCTCAGGGAACGTT
AGCTGACAGGAGGATGGTACGTGCTTCAGAAAGTGGAAAGCCACCAAGTTGTCACATCTCAGGTGCTGG
ATTTTCTTACACACATGACAGTAGTGGGACCTGCCATTGACAATAGCAGTGAAAGCTGATGTGGAAAGCTGC
CACAGATCTGTCCTTGTCCGTTTGGGATCCACAGGCCCTATGTTAGGAAAGGAAATGTTGATGGCTCAGA
TCCCTTTGAAACATATCATACAGGTTGCAGTCTGACCCAAAGACAGTTAATGGACCAACTATGAGCCAGTT
CATAAAGAAAAGGAGTGCTACCCATGTTCTCATCTTCAAGAACATCTGCCAGGGAGCTCAGTAATATATC
GTGGCCTTCACATGTGAGGAAGCTACTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAATCTGTG
TCTAAACAAGTCCTCTTAGTTAGTGCACATGCCAGAGCCAGCGTCGGTGCCTCGAGTAATTCTTCATGGG
TACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTGGACAGCCATCAGATTGTCAGCC
AAGGCCCTTTATTGAAAGCTCATTCTTCCAGACTTGGACTCTGGTCAAGAGAAGATGGAAAGAAAGGAC
AGATTTTCAGGAAGAAAATCACATTGACCTTAAACAGACTTTAGAAAATCAGGACTCCAAATTTCAGTC
TTATGACTGGACACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACACTCAAGTGAACTTTTATTTA
AAAGAGAGAGAATCTTATGTTAAATGGAGTTATGAATTAAAGGATAAAAATGCTTATTATACAGAT
GAACCAAAATTACAAAAAGTTATGAAAATTTTATACTGGGAATGATGCTCATATAAGAATAACCTTTTAAACTA
TTTTTTAACTTTGTTTATGCAAAAAAGTATCTACGTAATTAAATGATATAAAATCATGATTATTTATGTTATT
TTATAATGCCAGATTCTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCAATT
TTAAATAGAAGTTACTTCATTATTTGACACATTATTTAATAAAATGTCATTGAA

FIGURE 102

MVDVLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRIASIPPKMFKLPQLQHLELNRNKIKNDGLTFQGLGALKSLKM
QRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLYGILLMLQELHLSQNAINRISPDAWE
FCQKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDLKNNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSIKKAKFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWLPQWVAENNQSFVNASCAGHPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDPMTFAWKKDNELLHDAEMENYAHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLRTVKGETAVLQCIAGGSPPPQLNWTKDDSPVVTER
HFFAAGNQLLIIVDSVSDAGKYTCMSNTLGETRGNVRLSVIPTPTCDSPQMTAPSLODDG
WATVGVIIIAVVCVVGTSLVVVVIYHTRRRNEDCSITMTDETNLPADIPSYLSSQGTTLAD
RQDGYVSSESQSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDPFETYHTGCSPDPRTVLMHYEPSYIKKKECYPCHPSEESCRFSNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDSGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTGGTGGTGGCTGTTGGGTGCCTTGCAAAATG
AAGGATGCAGGACGCAGCTTCTCCTGGAACCGAACGCAATGGATAAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTTGAGGCCCTGGATCTAACACAATGTGTATATGTGACACACAGGGAGCATTCAAGAATGAAA
TAAACCAGAGTTAGACCCGCGGGGTTGGTGTGTTCTGACATAAAATAATCTAAAGCAGCTGTTCCCCTCC
CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCAACAAAGAAAAAGTATGTTCAATTTCCTC
TATAAAGGAGAAAGTGAGCCAAGGAGATATTGGAATGAAAAGTTGGGCTTTTAGTAAAGTAAGAAACT
GGTGTGGTGGTTCTTCTTGAATTCCCACAAGAGGAGAGGAATTAAATAACATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTGTGACCGCGGAGATTGAGGCATTGATTGGGGAGAGAACACAGCAGAGCACAGTTGGA
TTTGTGCCTATGTTGACTAAATTGACGGATAATTGAGTTGGATTTCTTCATCAACCTCTTTTTTAAAT
TTTATTCTTGGTATCAAGATCATGCGTTCTCTTGTCTTAACACCTGGATTTCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACGTGTTGAATTCCAAGGACCAACACCAGATAAAATTATGAATGTTGAAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCCCTGTTGGTGT
GCTGGCTTCAACTTCTGGTGGCTGGTGCAGGCTCAGACCTGCCCTCTGTGCTCCTGAGCAA
CCAGTCAGCAAGGTGATTGTGGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACGGCT
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCAGCTCAAGCAGCTGGAAATCCT
ACAGTTGAGTAGGAACCATACTAGAACCCATTGAAATTGGGGCTTCATGGTCTGGCAACCTCAACACTCTGGA
ACTCTTGACAATCGTCTTACCATCCGAATGGAGCTTGTATACTGTCTAAACTGAAGGAGCTGGTT
GCGAAACAACCCATTGAAAGCATCCCTCTTATGTTAACAGAACCTCTTGCGCCGACTAGACTTAGG
GGAATTGAAAAGACTTTCATACATCTCAGAAGGTGCTTGAAGGTCTGCCAACCTGAGGTATTGAACCTTGC
CATGTGCAACCTTGGAAATCCCTAACCTCACACCGCTCATAAAACTAGATGAGCTGGATCTTCTGGAAATCA
TTTATCTGCATCAGGCTGGCTTTCCAGGGTTGATGCACCTTCAAAACTGTGGATGATACAGTCCAGAT
TCAAGTGATTGAAACGAATGCCCTTGACAACCTCAGTCAGTCAGTGAGGATCAACCTGGCACACAATACTAAC
ATTACTGCCATGACCTCTCCTCCCTTGACATCATCTAGAGCGGATACATTTACATCACAAACCTTGGAACTG
TAACTGTGACATACTGGCTCAGCTGGTGGATAAAAGACATGGCCCTCGAACACAGCCTGTTGTGCGCGGTG
TAACACTCCTCCAACTCTAAAGGGGAGGTACATTGGAGAGCTGCACCGAGAACTACTCCTTACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAGGATGGCAGCTGAGTGAATGTGGGCTCAGCATC
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCAGTCAGACATGGGGCTACAAAGTGCAGGATAGCTGT
GCTCAGTGATGGTACGTTAAATTTCACAAATGTAACCTGTGCAAGATAACAGGATGTACACATGTATGGTAGTAA
TTCCGTTGGAAATACTACTGCTTCAGCCACCCCTGAATGTTACTGTGAGCAACCAACTACTCCTTCTTT
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGACGGACACAGATAACAAATGTGGTCCACTCC
AGTGGTCAGTGGAGACCACCAATGTGACCCACTCTCACACCAACAGCAGAACGGTGCAGAGAAAACCTT
CACCATCCCAGTGACTGATATAAACAGTGGATCCCAGGAATTGATGAGGTCTGAGACTACCAAAATCATCAT
TGGGTGTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCAATTCTACAAGATGAGGAAGCAGCACCA
TCGGCAAAACCATCACGCCAACAGGACTGTTGAAATTATAATGTGGATGATGAGGATACGGGAGACACACC
CATGGAAAGCCACCTGCCATGCCTGCTATGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT
CAACCAACACAACAGTTAACACAATAATTCAATACACAGTTGAGCTGATGAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAAAACAAACATCAAAAAAA
GACAGTTTATTAAAAATGACACAAATGACTGGCTAAATCTACTGTTCAAAAAAGTGTCTTACAAAAAAACAA
AAAAGAAAAGAAAATTATTAAATTCTATTGTGATCTAAAGCAGACAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFNDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHHNPWCNC
WLSWWIKDMAPSNTACCACNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVNSVGN
TTASATLNVTAAATTFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYN SYKSPFNHTTVNTINSIHSS
VHEPLLIRMN SKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTCGGTTTCCCTCCTGCTGTTGGGGCA
TGAAAGGGCTTCGCCGCCGGAGTAAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCGCACCGCACCGC
GAGGGCGGGCGTGCACCCCTCGGCTGGAAGTTGTGCCGGGCCCCGAGCGCGCCGGCTGGGAGCTTCGGGTAGA
GACCTAGGCCGCTGGACCGCG**ATGAGCGCGCCAGCCTCCGTGCGCGCCGCGGGTTGGGCTGCTGTGC**
GCGGTGCTGGGGCGCTGCCGACAGCGCGTCCGGAGCTCGGGACTCGGGCAGCCCTCTGGGTAGCGGCC
GAGGCCCATGCCCACTACCTGCCGCTGCCCTGGGACCTGACTGAGCTGAAGCGCTAGCGCGTCTT
CCCGAGCCACTCCGCTGGGTGACTTAAGTCACAACAGATTATCTTCATCAAGGCAAGTCC
ATGAGCCACCTCAAAGCCTCGAGAAGTGAACAAACATGAATTGGAGACCATTCAAATCTGGGACCA
GTCTCGGCAAATATTACACTTCTCTGGCTGAAACAGGATTGTTGAAACTCCCTGAACATCTGAAAGAG
TTTCAGTCCCTGAAACTTGGACCTAGCAGCAACAATATTCAAGAGCTCCAAACTGCATTCCAGGCCCTACAG
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGTATTGACAATTGGCCAACACA
CTCCTGTGTTAACGCTGAAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTAACACTGCCCAACTGCAA
CATCTGAATTGAACCGAAACAAGATAAAATGTAGATGACTGACATTCCAAGGCCCTGGTGTCTGAAAGTCT
CTGAAAATGCAAAGAAATGGAGTAAGAAACTTATGGATGGAGCTTTTGGGGCTGAGCAACATGAAATTGG
CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGTGATGCTGAGGAACATTGAT
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCTCAGTGAGCTGCC
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTCCTGGCTAAGCTTACTAAATACACTGCACATTGGG
AAACAACAGAGTCAGTACATTGCTGATTGTGCCCTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAAAGAAC
AATGAAATTCTGGACTATTGAAGACATGAATGGTGTCTCTGGGCTGACAAACTGAGGCAGTGATACTC
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTCACTGGTTGGATGATTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGTCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAATTGCAATTAAATACA
TCAAGGCTTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGGTGGCGAAAACAACACTTCAAGAGCTTGTA
AATGCCAGTTGTGCCCATCCTCAGCTGCTAAAGGAAGAACGATTGGCTTAGCCAGATGGCTTGTGTT
GATGATTTCCAAACCCAGATCAGGTTCCAGGAGAAACACAGTCCGCAATAAGGTTCCAATTGAGTTTC
ATCTGCTCAGCTGCCAGCAGCAGTGAATTCCCAATGACTTTGCTTGAAAGAACACAGTGAACACTG
GCTGAAATGAAAATTATGACACACCTCCGGGGCCAAAGGTGGCGAGGTGATGGAGTATACCAACATCCTCGGCTG
CGCAGGTGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAACACTTGGTTCATCCTACTCTGTC
AAAGCCAAGCTTACAGTAAATATGCTCCCTCATTCAACAGACCCCCATGGATCTCACCATCCGAGCTGGGCC
ATGGCACGCTTGAGTGTGCTGCTGGGGCACCCAGCCCCCAGATGCTGCCAGAAGGATGGGGCACAGAC
TTCCAGCTGCAGGAGAGACGCATGTCATGTGATGCCGAGGATGACGTGTTCTTATCGTGGATGTGAAGATA
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTCAGCAAATGCAACTCTGACTGTC
CTAGAAACACCATCATTGGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAACAGCCGCTCTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCATTGGTGGTAACCGAGAGGCAC
TTTTTGCAAGCAGGCAATCAGCTCTGATTATTGAGACTCAGATGTCAGTGATGCTGGAAATACACATGTGAG
ATGTCTAACACCTTGGCACTGAGAGAGGAAACGTGCGCTCAGTGTGATCCCCACTCCAACTCGGACTCC
CAGATGACAGCCCCATGTTAGACGATGACGGATGGGCCACTGTGGGTGCTGATCATAGCCGTGGTTGCTGT
GTGGGGGCCACGTCACTCGTGTGGTGGTCACTCATATACCACACAAGGGGGAGGAATGAAGATTGAGCATTAC
AACACAGATGAGACCAACTTGCCAGCAGATATTCTAGTTATTGTCATCTCAGGAAACGTTAGCTGACAGGAG
GATGGGTACGTGCTTCAGAAAAGTGGAGGCCACCAAGTTGTCACATCTCAGTGCTGGATTTCCTACCA
CAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAGCTGCCACAGATCTGTT
CTTGCCGTTGGATCCACAGGCCCTATGTTGAAAGGAAATGTGATGCTCAGATCCTTGTGAAACA
TATCATACAGGTTGCACTGCCATTCAAGCTTGGACGCCACTATGAGCCAGTTACATAAAGAAAAG
GAGTGCCTACCATGTTCTCATCCTTCAGAAGAAATCTCGCAAGGGAGCTCAGTAATATATCTGTC
GTGAGGAAAGCTACTAACACTAGTTACTCTCACAAATGAGGCCAGCGTGGCTCGAGTAATTCTTACGGTACCTTGG
TCTTTAGATTGCAATCCAGAGGCCAGCGTGGCTCGAGTAATTCTTACGGTACCTTGG
GCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACGCCACTAGATTGTCAGCCAAGAGCCTT
TTGAAAGCTCATTCTCCCCAGACTTGGACTCTGGTCAAGGAGATGGGAAAGAAAAGGAGCAGATTTCAGGAA
GAAAATCACATTGTACCTTAAACAGACTTTAGAAAATCAGGACTCCAAATTTCAGTCTTATGACTTGGAC
ACATAGACTGAATGAGACCAAGGAAAGCTAACATACACTACCTCAAGTGAACCTTATTAAAGAGAGAAT
CTTATGTTTTAAATGGAGTTATGAATTAAAGGATAAAAGCTTATTATACAGATGAAACCAAATTAC
AAAAGTTATGAAAATTAACTGGGAATGATGCTCATATAAGAATACCTTTAAACTATTAAACTTT
TTTATGCAAAAAGTATCTACGTAATTAAATGATATAATCATGATTATTGTTATGTTATATAATGCCAGA
TTCTTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCAATTAAATAGAAGTT
ACTTCATTATATTGCACTTAAATAAAATGTGCAATTGAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPQSGVAAERPCPTTCRCLGDILDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRIASAIAPPKMFKLQLQHLELRNKKNVDGLTFQQLGALKSLKMQR
NGVTKLMGAFWGLSNMELQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC
QKLSELDLTFNHLSRLDDSSFLGLSLLNLTIHGNRVSYIADCAFRLSSLKTLDLKNNIEIS
WTIEDMNGAFSGLDKLRLLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQQLHLNTSLLCDCQLKWLQPQWVAENNQSFVNASCAPOLLKGRSI FAVSPDGFCVDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCQAQNSA
GSISANATLTVLETPSFLRPLLRTVTKGTAVALQCIAGGSPPPKNWTKDDSPLVVTERHF
FAAGNQLLIIVDSDVSDAGKYTCMSNTLGTERGNVRLSVIPTPTCDSPQM TAPS LDDDGWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRNEDCSITNTDETNLPADIPSYLSQGTIADRO
DGYVSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEATDLFLCPFLGSTGPMY
LKGNVYGSDFETYHTGSPDPRTVLMHYEPSYIKKKECYPCHPSEESCRFSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTL ENY RTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGGGAGAGCGCCCAGCTTGACTTGAAATGGAAGGAGCCCGAGCCCGGGAGCGCAGCTGAGAC
TGGGGGAGCGCGTTCGGCCCTGTGGGGCGCGCTCGCGCCGGGCGCAGCAGGGAAAGGGAAAGCTGTGGTCTGCC
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCCCTGGGTGGTCCCGTCCCTATCCCTCCTTATATA
GAAACCTTCCACACTGGGAAGGCAGCGCGAGGGCAGGAGGGCTCATGGTGAGCAAGGAGGCCGCTGATCTGCAG
GCGCACAGCATTCCGAGTTACAGATTTACAGATAACCAATGGAGGCAGGAGGCAGAACAGCCTGCCCTGGT
TCCATCAGCCCTGGCGCCAGCGCATTGACTCGGCACCCCTGCAGGCACCATTGGCCAGAGGCCGGGTGCTGC
TGCTCCTGCTGCTGCCAACAGCTGCACCTGGACCTGTGCTTGGCGTGGAGGCCAGGATTTGCCGAA
GTGGCGGCCAACAGCCTGAGGCCGAAGAGAACGAATTTCGAGGAGGGAGGCCGCTGTGGTACTGAGCCCTGAGG
AGCCCGGGCCTGGCCCAGCCCGGGTCAAGCTGCCCTGGAGACTGTGCTGTCCAGGAGGGCCTGTGGACTGTG
GCGGTATTGACCTGCGTGAGTCCCGGGGACCTGCTGAGCACACCAACCCTATCTGCAGAACACCAGC
TGGAAAAGATCTACCCCTGAGGAGCTCTCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAAACACCCTGA
CTTCCCGAGGGCTCCCAGAGAACGGCTTGAGCATCTGACCAACCTCAATTACCTGACTTGCCAATAAACAGC
TGACCTTGGCACCCGCTTCTGCCAACGCCCTGATCAGTGTGGACTTGTGCAACTATCTACCAAGATCT
ATGGGCTCACCTTGGCCAGAACGCAAACTTGAGGTCTGTGACCTGACAAACAAAGCTGGCAGACGCCGGC
TGCGGACAACATGTTAACGGCTCCAGCAACGTGAGGTCTCATCTGTGCCAGCAACTCTGCGCACGTGC
CCAAGCACCTGCCGCTGCCCTGTACAAGCTGCACCTCAAGAACACAAGCTGGAGAAGATCCCCCGGGGCCT
TCAGCGAGCTGAGCAGCCTGGCGAGCTATACCTGAGAACAAACTACCTGACTGAGGGCCTGGACAAGAGA
CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAAACTGTCTGGGTCCCAGCTGGCTGC
CGCGCAGCCTGGTGTGCTGCACCTGGAGAACGCAAGGCTGGAGGCCAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGCTGCACAGCAACCAGCTGCCGGAGCAGGGCATCCACCCACTGCCCTCCAGGGCC
TCAAGCGGTTGCACACGGTGCACCTGATACAAACCGCCTGGAGCGCTGCCAGTGGCCTGCCCTGCGCTGC
GCACCCCTCATGATCTGCACACCAAGTACAGGATTGGCCCGAAGAGCTTGGCACCACCTACTCTGGAGG
AGCTCAACCTCAGCTACACCGCATTGGCCACAGGTGCAACCGCGACGCCCTCCGCAAGCTGCGCTGCTGC
GCTCGCTGGACCTGTGGGCAACCGGCTGCAACGCTGCCACCTGGGCTGCCCGAAATGTCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCCCTGGCACGAGGGCGCTGGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA
CCAGCAACCGACTGCGCAGCCGGAGGCCCTGGGCCCTGGGCTGCCCTGGGACCTGCCCATCTGAGCTGCTGGACA
TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGCTCCCCGAGTCACTTGAGTACCTGACCTGCAAACAACA
AGATTAGTGCCTGGTGGCCCAATGCCCTGCACTCCACGCCAACCTCAAGGGATTTCTCAGGTTAACAAAGC
TGGCTGTGGGCTCCGTGGTGGACAGTGCCTTCCGGAGGCTGAAGGCACCTGCAAGGTCTTGGACATTGAAGGCAACT
TAGAGTTGGTGAATTTCAAGGACCGTGGCCGCTTGGGGAGGAAAAGGAGGAGGAGGAGGAGGAGGAGG
AGGAAGAGGAAAAGATAGTGACAAGGTGATGCAAGTGTGACCTAGGATGATGGACCGGGACTCTTCTGC
AGCACACGCCCTGTGTGCTGAGCCCCCACTCTGCCGTGCTCACACAGACACACCAGCTGCACACATGAGGCA
TCCCACATGACACGGCTGACACAGTCTCATATCCCACCCCTGCCACGGCGTGTCCCACGCCAGACACATGC
ACACACATCACACCCCTAAAACACCCAGCTCAGCCACACACAACTACCCCTCAAACCACACAGTCTGTACAC
CCCCACTACCGCTGCCACGCCCTGTGAATCATGCAAGGGAAGGGCTGCCCTGCCACACACAGGCC
TTCCCTCCCCCTGCTGACATGTGATGCGTATGCATACACACCACACACACATGCACAGTCATGTGCGAA
CAGCCCTCCAAAGGCTATGCCACAGACAGCTTGGCCAGCCAGAATGCCATAGCAGCTGCCGTCTGCCCT
GTCCATCTGTCCGTCCCTGGAGAAGACACAAGGTATCCATGCTCTGTGGCCAGGTGCCACCCCT
GGAACTCACAAAGGCTGGTTATTCTTCCATCTATGGGACAGGAGCTCAGGACTGCTGCCCTGGCC
TGGCCACCCCTGCTCCCTCCAGGTGCTGGCGAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCACCTTCCAAAGGGAAGGCCAAGGCCAGTGGAGGCAGGATGGAGAGGCCCTGGGTGCTGCTGGGGCCTTGGGG
CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCCAGGGAGGAAGGACCCAGTCACCTAGGAGACACCTT
GTTCTCAGGCCCTGTGGGGAAAGTTCGGGTGCCCTTATTCTTATTCTTCTAAGGAAAAAATGATAAAAAAT
CTCAAAAGCTGATTCTTCTGTTAGAAAAACTAATATAAAGCATTATCCCTATGCCCTGCAAAAAAAAAA

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENFAEEEPLVLSPEEPGPAAVSCP RD CACS QEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEK IYPEEL SRLHRLETLN LQNNR L TS RGLPEKA FEHL TN NYLYL ANN K
LT LAPRFLPNALISV DFA ANYLT KIYGLTFQKPNLRSV YLHNNKLADAGL PDNM FNGSSNV
EV LILSSNFLRH VP KHL PP ALYKLHLKNNKLEK I PPGAFSELSSLRELYLQNNYL TDEGLDN
ET FWKLSSLEYLDLSSNNL SRVPAGLPRSLVLLHLEKNAIR SV D ANV LTP IRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLP RRVRTLMILHNQITGIGREDFATTYF
LEELNLSYNRITS PQVHRDAFRKLRLRSRLSGNR LHTLPPGLPRNVHVLKVKRNEAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQ LLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLK GIFLRFNKLAVGSVVD SAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCGGGCGCGCAGCAGACCTGCTCCGGCCGCGCCTGCCGCTGTCCCTCGGGAGCGGCAG
CAGTAGCCCCGGCGCGAGGGCTGGGGTTCCTCGAGACTCTCAGAGGGCGCCTCCATGGCGCCACCACCC
CAACCTGTTCTCGCGCGCACTGCGCTGCGCCAGGACCCGCTGCCAACATGGATTCTCCTGGCGCTGGT
GCTGGTATCCTCGCTCTACCTGCAGGGGCCCGAGTCAGGGAGGTGGCCCAGGCAAATAGTGTATCGAT
TGGCCTATGTCGTTATGGGGAGGATTGACTGCTGCTGGGCTGCCAGCTTGGAACAGTGTCAAGGCC
TGTGTGCCAACACAGATGCCAACATGGTAATGTATCGGGCCAACAAGTGCAGTGTCACTCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGCCCCGGCCCTGTAAGCACAGGTGCATGAACACTTA
CGGCAGCTACAAGTGTCACTGTCAGGGATAATGCTCATGCCGGATGGTCCCTGCTCAAGTGCCTGACCTG
CTCCATGGCAAACACTGTCAGTGGCTGATGTTAAAGGACAATACGGTGCAGTGCCATCCCCCTGGCCT
GCACCTGGCTCTGATGGGAGGACCTGTGATGTTAAAGGACAATACGGTGCAGTGCCATCCCCCTGGCCT
TAGGCAATGTCACACTTTGGGAGCTACATGCAAGTGTCAAAAGGCTTCGATCTCATGTATATTGGAGG
CAAATATCAATGTCATGACATAGACGAATGCTCACTGGTCAGTATCAGTGCAGCAGCTTGCTCGATGTTAA
CGTAGCTGGCTCTACAAGTGCACATGGTAAAGAAGGATACCGGGTGTGGACTGACTTGTGTATATCCCCAA
AGTTATGATTGAACTTCAGGTCCAATTGATACAAAGGGAAATGGTACCAATTAAAGGGTGACACAGGAAA
TAATAATTGGATTCTGATGTTGGAAAGTACTTGGTGGCTCCGAAGACACCATATATTCTCTATCATTACCAA
CAGGCCTACTTCTAAGCCAACAACAAGACCTACACCAAAGCCAACACCAATTCCACTCCACCAACCACC
CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAAGGCCAACACCAGGACTGACAACATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGACAGCCCTCAGAAACCCAGG
AGATGTTGTCAGTGTCTGGTACACAGTTGTAATTGACCATGGACTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACTGGAACCAATCAGGGACCAGCAGGTGGACAATATCTGACAGTGTGGCAGGCCAAGCCCCAGG
GGGAAAGCTGCAGCTGGTGTACCTCTGGCCCTCATGCATTAGGGACCTGTGCCGTGATTAGGGCA
CAAGGTGACGGGCTGCACTCTGGCACACTCCAGGTGTTGTGAGAAAACACGGTGCCACGGAGCAGCCCTGTG
GGGAAGAAATGGTGGCCATGGCTGGAGGAAACACAGATCACCTTGCGAGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAAGGGTTGGAAAAAAAGATCTATGATGGAAATTAAAGGAACCTGGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGCAAACCAATTGATGGTTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCACCAGCTG
TTCTCCATATGCACTAAGAATAGAACAGAGGAAACTGGCTAGACTAGAGTATAAGGGAGCATTCTGGCAGG
GCCATTGTTAGAATACTTCATAAAAAAGAGTGTGAAAATCTCAGTATCTCTCTCTTCTAAAGGAAATTAGA
AAAAAATTGTCATTAAAGATGGTTAAAGATGTTCTACCAAGGAAAGTAACAAATTATAGAATTCCCCAA
AGATTTTGATCTACTAGTAGTATGCACTGAAATCTTAAAGACTAATAATTGGACAAGGCTTAATTAGG
CATTTCCCTTGTGACCTCTAATGGAGAGGGATTGAAAGGGCAAGGCCACAAATGCTGAGCTCACTGAAATA
TCTCTCCCTATGGCAATCTCAGTATTAAAGAAAAAGGAAACTATTATTCACAAATGAGAGTATGATGGAC
AGATATTAGTATCTCAGTAATGTCCTAGTGTGGCGGTGTTCAATGTTCTCATGGTAAAGGTATAAGCC
TTTCATTGTCATGGATGATGTTCAAGATTGTTTTTAAGAGATCTCAAGGAACACAGTTCAGAGAG
ATTTTCATCGGGTGCATTCTCTGCTTGTGACAAGTTATCTGGCTGCTGAGAAAGAGTGCCTGCC
ACACGGCAGACCTTCTCACCTCAGTATGATTGAGTTCTCTTCAATTGGACTCTCCAGGGTCCAC
AGAACAGTAATATTTTGAAACAATAGGTACAATAGAAGGTCTCTGTCATTAACTGGTAAAGGCAGGGCTGG
AGGGGAAAATAATCATTAAGCCTTGGAGTAACGGCAGAATATGGCTGTAGATCCATTAAATGGTTCAATT
TCCTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGAAAATAATGAAAATTTCATTTGATGCCAA
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTATTATTAATGGTT
CTAAAATAAAATGTTAGTGGTTTCCAATGGCTAATAAAACAATTATGTAATAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCFKRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDDVVKGQIRCQCPSPGLHLAPDRTCVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMLYIGGKYQCHDIDECSLGQYQCSSFARCYNRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKDTGNNNWI PDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPPTPPPPPPLPTELRTPLPPTPERPTTGLTTIAPAASTPPGGITVDN
RVQTDPKPRGDVFSLVHSCNFHDGLCGWIREKDNDLHWEPIRDPAQQYLTVSAAKAPGG
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACTTCCCTTGCAACAGGTGCTCGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTACCTACCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATGGCTATTGAGAGACCCCA
ACAATGCCAAATACTTACTGGCTCTGTGAATAAGTCTGTGGTCCCTGACTTGAATACC
AACACAAGTTACCATGATGCCACCCAAATGCATCTGTCCATTCAACCCACTGCAGTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTAGGGAAATGGAACTCTATCTGCCAGTCA
GAAGATAACAAGTCACGGTGATGATCCTGTACAAAGCCAGTGGTGCAGATTCACTCCTCCCT
CTGGGGCTGTGGAGTATGTGGGAACATGACCTGACATGCCATGTGGAAGGGGGACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTCT
TCCCCAAAACAATACCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGAATTACAGCT
GCCTGGTGAGGAACCTGTCAGTGAAATGGAAAGTGATATCATTATGCCCATCATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTACTGT
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAAGCATGGGCTCGCTTAGAAGTT
GCATCTGAGAAAGTACCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAACTCATTCACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAATCATTGTCACCTTAGCAAGTATAACTGGAATATCACTATTTGATT
ATATCCATGTCTTCTTCTTCTATGGAAAAAAATATCAACCCCTACAAAGTTAAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATGAATTGTTGCTTCCAGATGTTCTGGTGTCCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGATCGGGCAAGATTGACAGTACAGT
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATCCAGAGTGAACCTTCATGG
GCTAAACAGTACATTGAGTGAAATTCTGAAGAAACATTAAAGGAAAACAGTGGAAAAGT
ATATTAATCTGGAATCAGTGAAGAAACAGGACCAACACCTCTTACTCATTATTCTTACA
TGCAGAATAGAGGCATTATGCAAATTGAACTGCAGGTTTCAGCATATAACAAATGTCTT
GTGCAACAGAAAAACATGTTGGGAAATATTCCCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGTTCTCATAAGTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAAACTTACATTGTTGCAATTTCAGCAGACTTGTGTTATTAAATTGTTATTAGTG
TTAAGAATGCTAAATTATGTTCAATTTCAGGAAATTCTATCTGTTATTGTACAA
CAAAGTAATAAGGATGGTTGTCAAAAAACAAAATAGCCTCTTTTTCAATCACC
AGTAGTATTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA
TTTTTTCAAGGAAAGATGGATTCAAATAATTCTGTTTGCTTTAAAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSSHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLSASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRTDNTTYIIKGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPTEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPRSVPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGC~~AA~~**ATGGCGCCCTCCGGGAGTCTTGCAGTTCCCCTGGCAGTCCTGGT**GCTGTT
GCTTGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAAGGAGACTGGATGATAGAATTATGCCCGTGGTGCCTGCT
TGTCAAATCTCAACCGGAATGGAAAGTTGCTGAATGGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTTATCATTGTAAGATGGTGAATTAGGCCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGCCGTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCAGTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGATCATATACT
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCCTTGTCTCCTCAAAAAGGCCAGACCACAGCCATACCCATACCCCTCAAAAAAAT
TATTATCAGAATCTGACAACCTTGAAAAAAGTGGAGGAGGAACAAGAGGCCAGTGAAGAA
GATGTTTCAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAACATGC
CATAAAGACAAACGCTCTGGTCCATCATTGCCACAGATAATCTAGTTAAATTATAG
TTATCTTAATATTGATTTGATAAAAACAGAAAGATTGATCATTGTTGGTTGAAGTG
AACTGTGACTTTTGAAATATTGCAAGGTTCACTGAGTTGAAATATGATTAAAGAGTCTA
CATTAGAACATAAAAGCACTAGGTATACAAGTTGAAATATGATTAAAGCACAGTATGATG
GTTTAAATAGTTCTAATTGAAAAATCGTGCCTAACAGCAATAAGATTATGTATATTGT
TTAATAATAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAAGTATTGCAATT
TGAGGTATTTAAGAAGATTATTAGAGAAAATTCTCATTGATATAATTCTCTG
TTTCACTGTGAAAAAAGAACATATTCCATAAATGGGAAGTTGCCATTGCTCAAG
AAATGTGTATTCAGTACAATTCTGGTCTTTAGAGGTATATTCCAAAATTCTTGT
ATTAGGTTATGCAACTAAATAAAACTACCTTACATTAAATTACAGTTCTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTAAGTCTGGTATTCTTGT
CAACAAAGTTGATTTCTTGTATTCTTACTTACTATGGTTACATTTTTATT
CAAATTGGATGATAATTCTGGAAACATTATGTTAGTAAACAGTATTGTTGTT
GTTTCAAACGTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTAAAATT
TTGGCCACTTTTCAGATTTACATCATTCTGCTGAACCTCAACTGAAATTGTTTTT
TTTCTTTGGATGTGAAGGTGAACATTCTGATTTGTCTGATGTGAAAAAGCCTGGTA
TTTACATTGAAAATTCAAAGAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAG
CATCTTCTGTATATGTCTTAAATGTATTGTCCTCATATACAGAAAGTCTTAATTGAT
TTTACAGTCTGTAATGCTGATGTTAAATAACATTATTTATATTGTTAAAAGACAA
ACTTCATATTATCCTGTTCTTCTGACTGGTAATTGTTGTTGGGATTCACAGGTAAA
GTCAGTAGGATGGAACATTAGTGTATTCTACTCCTAAAGAGCTAGAATACATAGTTT
CACCTTAAAGAAGGGGGAAATCATAAATACAATGAATCAACTGACCATTACGTAGTAGAC
AATTCTGTAATGTCCCTTCTTAGGCTCTGTTGCTGTGAATCCATTAGATTACAG
TATCGTAATATACAAGTTCTTAAAGCCCTCTCCTTAGAATTAAAATATTGTA
AAAGAGTTGGATGTGTAACCTGTTGATGCCCTAGAAAATATCCTAAGCACAAACCT
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVT EQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGS VLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCP SKRRRPQPYPYPSKKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCGTGATAATTGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTGTAACCCAGTGGACAGGGGGATTGGAAGAGCGGG
AAGGTCTGGCCCAGAGCAGTGTGACACTTCCTCTGTGACC**ATGAAACTCTGGGTGTCTGC**
ATTGCTGATGGCCTGGTTGGTGTCTGAGCTGTGAGGGCGAATTCTCACCTCTATTG
GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGCCAACAAAATGGAAGCCTTGAC
TAGCAAGTCAGCTGATGCTGAGGGTACCTGGCTACCCCTGTGAATGCCTACAAACTGG
TGAAGCGGCTAAACACAGACTGGCTGCGCTGGAGGACCTGTGAGGACTCAGCTGCA
GGTTTATGCCAACCTCTGTGAGCGGGCAGTTCTCCCCACTGATGAGGAGCAGAGATAGG
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGAACTTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG
GGCCGCTCGGCCTACAATGAAGGGACTATTATCATACTGGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGTCCTCAGTTGGTGTGACCTGCACCGTGCCTGGAGCTCACCGCCGCTGCTC
TCCCTGACCCAAGCCACGAACGAGCTGGAGGAACTGCGGTACTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCAGAAGGCA
TCTATGAGAGGCCCTGGACTACCTGCTGAGAGGGATGTTACGAGAGCCTCTGCGTGG
GAGGGTGTCAAACGTACACCCCCTAGACAGAAGAGGTTCTGTAGGTACCAACCATGGCAA
CAGGGCCCCACAGCTGCTCATTGCCCTCAAAGAGGAGGACGAGTGGACAGCCGCACA
TCGTCAGGTACTACGATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
CCTAAACTTGACGAGGCCACCGTGTGATCCAAGACAGGAGTCTCACTGTCGCCAGCTA
CCGGTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCCCTGTTGTGGCCGAGTAAATC
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT
TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTGACAGCGG
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATACATGAGTGTAGAAGCTG
GTGGTGCACCGTCTTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTGCGAGCGGGGAAGGTGACTACCGAACAAAGACATGCTGCC
TGTGCTTGTGGCTGCAAGTGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAAACAGAAGTTGACT**TGAC**ATCCTTCTGTCCTTCCCTCGTC
CTTCAGCCCAGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGAGACCATACTAGGGCGACTCCTGT
GTGACTGAAGTCCCAGCCCTTCATTAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
AAAGTGGCTGCAGCAGAGTTAGCTGTAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTT
TTAGGGTGTGAGATGTTCACTGAACCAAAGTTCTGATACCTTGTACATGTTGTTTAT
GGCATTCTATCTATTGTGGCTTACCAAAAAATAAAATGTCCCTACCAAGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPAGEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGDDYYHTV
LWMEQVLKQLDAGEATTKSQVLDYLSYAVFQLGDLHRAELTRRLLSLDPSHERAGGNLR
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVDPYLPERDVYESLCRGEVKLTPRRQKRLF
CRYHGHNRAPQLLIAPFKEEDEWDSPHIIVRYDVMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVAWSYRVSKSSWLEEDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEDDYR
TRHAACPVLVGCKWVSNKFHERGQEFLRPCGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTTCCTCTTTAGGGAAGACAGACCATAATCCAGTGTGAGTGAAATTGATTGT
TTCATTATTACCGTTTGGCTGGGGTAGTTCCGACACCTCACAGTGAAGAGCAGGAGAAGGAGTTGTGA
AGACAGGACAATCTCTGGGATGCTGGTCTGGAAGCCAGCGGGCTTGCTCTGTCTTGGCCTCATGACCC
CAGGTCTCTGGTAAAGCTACTACTGGCCTGGTCCCCTCAATCCATTGATCCTTGAGGCTGTGCC
CCTGGGCACCCACCTGGCAGGGCTTACCACT**ATG**CGACTGAGCTCCCTGTTGGCTCTGTCGGCCAGCGCTTC
CCCTCATCTTAGGGCTGTCTCTGGGGTGAGCCTGAGCCTCTGCGGGTTCTGGATCCAGGGGAGGGAGAAG
ATCCCTGTGTGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG
ATGAAGACTTCAAACCCCGATTGTCCCCTACTACAGGGACCCAAAGCCCTACAAGAAGGTGTCAGGACTC
GGTACATCCAGACAGAGCTGGCTCCCGTGAGCGGTTGCTGGCTGTGACCTCCGAGCTACACTGTCCA
CTTGCGCTGGCTGTGAACCGTACGGTGGCCCATCACTTCCCTCGGTTACTCTACTTCAGTGGCAGCGGGGG
CCCAGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGATGAGCGGCCGCTGGCTCATGTCAGAGACCCCTGC
GCCACCTTCACACACACTTGGGCCACTACGACTGGTTCTCATCATGCAGGATGACACATATGTGCAGGCC
CCCAGGCTGGCAGGGCTTGTGGCCACCTCAGCATCAACCAAGACCTGACTTAGGCCGGCAGAGGAGTCATTG
GCGCAGGGCAGCAGGCCGGTACTGTCTGGGGCTTGGCTACCTGTCACGGAGTCTCTGCTTCGTCTGC
GGCCACATCTGGATGGCTGCCAGGGAGACATTCTCAGTGGCCCTGACGAGTGGCTGGACGCTGCCCTCATTTG
ACTCTCTGGCGTGGCTGTCTCACAGCACCAGGGCAGCAGTATCGCTCATTGAACTGGCCAAAATAGGG
ACCCCTGAGAAGGAAGGGAGGCTGGCTTCTGAGTGCCTCGCCGTGACCCCTGTCAGGAAGGTACCCCTCATGT
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGGTTACAGTGAATAGAACAACTGCAGGCTCAGA
TCCGGAACCTGACCGTGTGACCCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCGTGGCTCCCTGCTCTTCA
CACCAACTCTCGCTTGAGGTGCTGGCTGGACTACTTCACAGAGCAGCACACCTCTCTGTGAGATGGGG
CTCCCAAGTGCCACTACAGGGGCTAGCAGGGCGACGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGCGCTATCAGCCCCGCTGCGCTTCCAGAACGAGCAGCGACTGCTCAACGGCTATCGCGCTTCGACCCAGCAC
GGGGCATGGAGTACACCCCTGGACCTGCTGTTGGAAATGTGTGACACAGCGTGGGACCCGGGGCTGGCTCGCA
GGGTCAAGCCTGCTGCGGCCACTGAGCCGGTGGAAATCCTACCTATGCCCTATGTCAGTGGCCACCCAGTGC
AGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGAGCCCCGGCTTCCCTGAGGGCTTGAGCCAATGTCC
TGGAGGCCACGAGAACATGCTACCCCTGTTGCTGAGTCAATCTGCCCCGTGACCCACAGAGATCACCCCCAGGGCCCC
ACCCATTCTTGGGGTAGGGCTGCAGCAGCGAGTTAGAGCGACGGTACCCCTGGGACGAGGTGGCTGGCTGGCTCG
CTGTGCGAGCAGGGCCCTTCCAGGTGCGACTCATGGACGTGGTCTCGAAGAACGACCCCTGTGGACACTCTCT
TCTTCCCTTACCCACCGTGTGGACAAGGCTGGCCGAAGTCTCAACCGCTGTCGATGAATGCCATCTGGCT
GGCAGGCCCTTCCAGTCCATTCCAGGAGTTCAATCTGCCCCGTGACCCACAGAGATCACCCCCAGGGCCCC
CGGGGGCTGGCCCTGACCCCCCTCCCCCTGGTGTGACCCCTCCCCGGGGCTCTATAGGGGGAGATTG
ACCGGCAGGCTTCTGGAGGGCTGCTTCTACACGCTGACTACCTGGGGCCGAGCCGGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGGCCCTGGAGGGCTGGAGGTGATGGATGTTTCCCTCCGGTTCTCAGGGCTCC
ACCTCTTCTGGGCCGTAGAGGCCAGGGCTGGTGCAGAACAGTTCTCCCTGCGAGACTGCAAGGCCACGGCTCAGTGAAG
AACTCTACCACCGCTGCCGCTCAGCAACCTGGAGGGCTAGGGGGCGTGGCTATGGCTCTTGTGAGGCC
AGCAGGAGCAGGCCAATAGCACT**TAG**CCCGCTGGGGCCCTAACCTCATTACCTTCTGGCTGTATTAAATGAAATGTTATTAA
ACATGTCTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD
QSDEDFKPRIVPYYRDPNPKPYKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLA
AHHPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEFIGAGEQARYCHGGFGYLLSRSLLLRPHLDGCRG
DILSARPDEWLGRCLIDS LGVGCVSQHQQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTP
HGWDYFTEQHTFSCADGAPKCPLQGASRADVGALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMETYLDLLECVTQRGHRRALARRVSLLRPLSRVEILPMYVTEATRVQLVLP
VAEAAAAPAFLEAFAANVLEPREHALLTLLL VYGPREGGRGAPDPFLGVKA
AAAEELERRYPG
TRLAWLAVRAEAPSQVRLMDVVKHPVDTLFFLTWTRPGPEV
NRCRMNAISGWQAFFP
VHFQEFPALSPQRSPGPPGAGPDPPSPGADPSRGAPIGGRFD
RQASAEGCFYNADYLAA
RARLAGELAGQEEEEALEGLEVMDVFLRFSGLHLFR
AVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRQLAMALFEQEANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCACACGTGAGAGGAACCGTGCACGGCTGCCTTCCTGTCCCCAAGCC
GTTCTAGACGCCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTTGG
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGCTGCAGTAAAGGAGACTTGGACCAACACTGTGACAAAGCAG
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTGATAAGTATAGAGACCAATACAAC TG
GTTCTCCTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTTGTTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTAATACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC
CAACCAGGTAGTAGAAGGCTGTTAGATGGCTGTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGTGATGGGTATACGCCCTAGGGCATTGGCATATTTCAAT
GATGCATTGGTTTCTACCTCAAATGGTCTGACAATGACTGAAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTGTCATTATTGTAGTAGTAACATACATATCCAA
TACAGCTGTATGTTCTTTCTTTCTAATTGGTGGCAGTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTTAAAACACATGAACATTGAAATG
TGTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAACTATTAAATAATATTAT
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGCACATATTTGCTGATTGGTT
AAAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACCTTGTGTTCCCTTACTTCTAATACTGATTTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTGCGCTCTCAAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAGTGGAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNDMWLMRK
AYKYAFDKYRDQYNWFFLARPTTFAIENLKYFLKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCACCGCGTCCGATCTTACCAACAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAACAAAAACCAAAGAGAGAGAAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTTCTTCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCCTATTCTCAGTGCCTGTTCATCACAGATGTGTTGTGACATTCGCAT
CTTCAAAACCTGTGATGAGAAAAGTTCAGCTACCTGAGAATTCACAGAGCTCTGCT
ACAATTATGGATCAGGTTCAAGAATTGTTGCCATTGAACTGGGAATATTTCAATCC
AGCTGCTACTTCTTTCTACTGACACCATTCCCTGGCGTTAAGTTAAAGAACTGCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCCTTACAAGA
AACCTAAAATGAGAGAGTTTTTATTGGACTGTCAGACCAGGTTGTCAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTCTGGATGTAGGGAGGCCAACAA
CATAGCTACCCTGGAGGACTGTGCCACCATGAGAGACTCTCAAACCCAAGGCAAAATTGGA
ATGATGTAACCTGTTCTCAATTATTTGGATTGTGAAATGGTAGGAATAATCCTTG
AACAAAGGAAAATCTCTTAAGAACAGAAGGCACAACCAAATGTGAAAGAAGGAAGAGCA
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTGTGCGCTGAACCTCAAAGGACTTC
ATAAGTATTGTTACTCTGATACAAATAAAATAAGTAGTTAAATGTTAAAAAAAAAAAAAA
AA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCNYGGSVKNCCPLNWEYFQSSCYFFSTDТИSWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCCGACATGGCGCTGAGGCAGGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCCTGACTCTTCCTGCTGCTGTTCAAGGGCTGCCTGATAAGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCCAGTGGTACAGGAATTGAAAGTGTGAACTGTCTGCATCATTACGGATTGCG
AGACAAGTGACCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAAA
TTCAGGGAGACTTGGCGGGTCTGCAAGAAATACTGGGAAGACATCCCTGAAGATCTGAATGTGACACGGAGAG
ACTCAGGCCCTTATCGCTGTGAGGTCGTTGCTGAAATGACCGAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGCTGTAGAGTGCCGAAGGCTGTACCTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCACCCCCGGCCTACTACAGCTGGTATCGCAATGTGATGACACTGCCACGGATT
CCAGAGCCAATCCCAGATTTCGCAATTCTCTTCCACTTAAACTCTGAACACAGGCACTTGGTGTCACTGCTG
TTCAAGGACGACTCTGGCAGTACTACTGCATTGCTTCAATGACCGCAGGCTCAGCAGGTTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGTCTGGTTGCTCTGCTACTGGCCCTGA
TCACGGTGGGATCTGCTGTGATCACAGACGTGGCCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACCAAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCACTTCAGACACAAGTCATCGTTG
TGATCTGA GACCCCGGGTGGCTGAGAGCGCACAGAGCGCACGTGCACTACCTCTGCTAGAAAACCTCTGCTAA
GGCAGCGAGAGCTGATGCACTGGACAGAGCTAGACACTCATCAGAAGCTTTCTGTTGGCAAAGTTGACCA
CTACTCTCTTACTCTAACAGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAATATAACCACAA
GGAAGCGAAACTGGGTGCGTTACTGAGTTGGGTTCTTAATCTGTTCTGGCCTGATTCCGATGAGTATTAGG
GTGATCTAAAGAGTTGCTCACTGAAACGCCGTGCTGGGGCTGTGAAGCCAGCATGTTACCACTGGTCGTT
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGGTGGCTGGACAGCACCAGCAGCGCATCCGGGGAAACCA
GAAAAGGCTTCTTACACAGCAGCCTACTTCATCGGCCACAGACACCACCGCAGTTCTTCTAAAGGCTCTG
TGATCGGTGTTGCACTGTCATTGGAGAGCTTTGGATCAGCATTTGTAAGAACACAAAATCAGGAAG
GTAATTGGTTGCTGGAAGAGGGATCTGCTGAGGAACCTGCTTGTCAACAGGGTGTCAAGGATTAAGGAAA
ACCTTCTCTTAGGCTAACTGAAATGGTACTGAAATATGCTTTCTATGGGTCTTGTATTAACTTAAACCTTAA
TACATCTAAATTGGTCAAGGATGTATTGATTATTGAAAGAAATTCTATTAAACTGTAATATATTGT
CATACAATGTTAAATAACCTATTGGTAAAGGTTCAACTTAAGGTTAGAAGTCTCAAGCTACTAGTGTAAAT
TGGAAAATATCAATAATTAAAGAGTATTGTTACCAAGGAATCTCATGGAAGTTACTGTGATGTTCTTTCT
CACACAAGTTTAGCCTTTTCACAAGGAACTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAATTCAGGTTAAAGCAATGTTGAAATCAGTTGCTCTTCAAAAGAAACCTCTCAGGTTAGCTTGAACCT
GCCTCTCCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGGCCCTCAGATGTACATACACAGATG
CCAGTCAGCTCTGGGGTGGCCAGGGCGCCCCCTGCTACTGCTACTGTTGCTCTGCTGCTGCCAGGAGGCCCT
GCCATCCTTGGGGCTGGCAGTGGCTGTCCCAGTGAAGCTTACTCAGCTGGCCCTTGCTTCAACAGCACAGC
TCTCAGGTGGGACTGCAAGGACACTGGTGTCTTCCATGTCAGCTGCCAGCTTGGGCTCTGTAACAGACCTCT
TTTGTTATGGATGGCTCAAAAATAGGGCCCCAATGCTATTGTTTAAGTTGTTAAATTGGTT
AAGATTGCTAAGGCCAAGGCAATTGGAAATCAAGTCTGTCAGTACAATAACATTGTTAAAGAAATGGAT
CCCACTGTTCTCTTGCACAGAGAACCCAGACGCCACAGGCTCTGCGCATTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCTGGGGAGGAAAG
TGAAACGCCCTGAATCAAAGCAGTTCTAAATTGACTTTAATTTCTATCCGGGGAGACACTGCTCCATT
TGTGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCCTGGA
GAATGGCTCTCACTACTCACCTGTCTTCAGCTCCAGTGTCTTGGGTTTTTATACTTGTGACAGCTTTTTT
AATTGCTACATGAGACTGTGTTGACTTTTGTATTGAAACACTTGCCTGCCAGGCCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGTCCCTGGTGTCTGCATGGCATCCTGGATGCTAGCATGCAAGTTC
CCTCCATCATTGCCACCTTGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTTGGGATTACCGCTCCAGCCTCCT
TCTTGGTTGTCTAGTGTAGGGTAGCCTTATTGCCCTCTTCTTAAACCTCTACACTAGTGCCTA
TGGGAACCAAGGTCTGAAAAAGTAGAGAGAAGTGAAGACTAGAGTCTGGGAAGTAGCTGCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTTAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATTATAAAAGCTTCAAAAAACCCA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAHPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267